

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: November 10, 2003, 06:16:09 ; Search time 446 Seconds

(without alignments)
95.887 Million cell updates/sec

Title: US-09-503-387-9

Perfect score: 1304

Sequence: 1 QSGPLPKPSIQALPSSLVPL.....SPKESDSPAGPARQYTKGN 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 644079 seqs, 171749292 residues

Total number of hits satisfying chosen parameters: 644079

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description |
|------------|-------|-------------|-----------|-------------------|-------------------|
| 1 | 1304 | 100.0 | 249 | US-09-832-312-9 | Sequence 9, Appl1 |
| 2 | 1304 | 100.0 | 319 | US-09-832-312-5 | Sequence 5, Appl1 |
| 3 | 1304 | 100.0 | 339 | US-09-832-312-3 | Sequence 3, Appl1 |
| 4 | 1304 | 100.0 | 339 | US-10-157-031-387 | Sequence 387, App |
| 5 | 1304 | 100.0 | 369 | US-10-446-826-37 | Sequence 37, App |
| 6 | 1300 | 99.7 | 339 | US-09-832-312-34 | Sequence 34, Appl |
| 7 | 1300 | 99.7 | 339 | US-09-832-312-36 | Sequence 36, Appl |
| 8 | 1300 | 99.7 | 339 | US-09-832-312-38 | Sequence 38, Appl |
| 9 | 1300 | 99.7 | 339 | US-09-832-312-40 | Sequence 40, Appl |
| 10 | 1277 | 97.9 | 339 | US-10-446-826-5 | Sequence 5, Appl1 |
| 11 | 895.5 | 68.7 | 267 | US-09-832-312-19 | Sequence 19, Appl |
| 12 | 895.5 | 68.7 | 292 | US-09-832-312-18 | Sequence 18, Appl |
| 13 | 895.5 | 68.7 | 313 | US-09-832-312-16 | Sequence 16, Appl |
| 14 | 895.5 | 68.7 | 313 | US-09-832-312-48 | Sequence 48, Appl |
| 15 | 891.5 | 68.4 | 313 | US-09-832-312-42 | Sequence 42, Appl |

| | | | | | | |
|----|-------|------|-----|----|-------------------|-------------------|
| 16 | 891.5 | 68.4 | 313 | 9 | US-09-832-312-44 | Sequence 44, Appl |
| 17 | 891.5 | 68.4 | 313 | 9 | US-09-832-312-46 | Sequence 46, Appl |
| 18 | 418 | 32.1 | 447 | 10 | US-09-870-759-50 | Sequence 50, Appl |
| 19 | 418 | 32.1 | 447 | 12 | US-09-751-708A-50 | Sequence 50, Appl |
| 20 | 418 | 32.1 | 448 | 12 | US-10-143-618-18 | Sequence 18, Appl |
| 21 | 418 | 32.1 | 448 | 15 | US-10-139-662-18 | Sequence 18, Appl |
| 22 | 418 | 32.1 | 448 | 15 | US-10-139-683-18 | Sequence 18, Appl |
| 23 | 411 | 31.5 | 447 | 11 | US-09-978-418-36 | Sequence 36, Appl |
| 24 | 408.5 | 31.3 | 632 | 12 | US-10-114-153-92 | Sequence 92, Appl |
| 25 | 405.5 | 31.1 | 631 | 9 | US-09-832-312-12 | Sequence 12, Appl |
| 26 | 400.5 | 30.7 | 631 | 12 | US-10-143-618-20 | Sequence 20, Appl |
| 27 | 400.5 | 30.7 | 631 | 15 | US-10-139-662-20 | Sequence 20, Appl |
| 28 | 400.5 | 30.7 | 631 | 15 | US-10-139-683-20 | Sequence 20, Appl |
| 29 | 399 | 30.6 | 590 | 12 | US-10-143-618-22 | Sequence 22, Appl |
| 30 | 399 | 30.6 | 590 | 15 | US-10-139-662-22 | Sequence 22, Appl |
| 31 | 399 | 30.6 | 590 | 15 | US-10-139-683-22 | Sequence 22, Appl |
| 32 | 398.5 | 30.6 | 489 | 12 | US-10-143-618-14 | Sequence 14, Appl |
| 33 | 398.5 | 30.6 | 489 | 15 | US-10-139-662-14 | Sequence 14, Appl |
| 34 | 398.5 | 30.6 | 489 | 15 | US-10-139-683-14 | Sequence 14, Appl |
| 35 | 396 | 30.4 | 466 | 10 | US-09-944-807-12 | Sequence 12, Appl |
| 36 | 396 | 30.4 | 483 | 12 | US-10-143-618-16 | Sequence 16, Appl |
| 37 | 396 | 30.4 | 483 | 15 | US-10-139-662-16 | Sequence 16, Appl |
| 38 | 396 | 30.4 | 483 | 15 | US-10-139-683-16 | Sequence 16, Appl |
| 39 | 388.5 | 29.8 | 289 | 12 | US-10-143-618-12 | Sequence 12, Appl |
| 40 | 388.5 | 29.8 | 289 | 15 | US-10-139-662-12 | Sequence 12, Appl |
| 41 | 388.5 | 29.8 | 289 | 15 | US-10-139-683-12 | Sequence 12, Appl |
| 42 | 385.5 | 29.6 | 431 | 15 | US-10-290-631-14 | Sequence 14, Appl |
| 43 | 385.5 | 29.6 | 431 | 15 | US-10-290-631-20 | Sequence 20, Appl |
| 44 | 385.5 | 29.6 | 598 | 12 | US-10-143-618-10 | Sequence 10, Appl |
| 45 | 385.5 | 29.6 | 598 | 15 | US-10-139-662-10 | Sequence 10, Appl |

ALIGNMENTS

| | | | |
|---------------------------------------|----|--|-----------------------------------|
| RESULT 1 | | US-09-832-312-9 | |
| ; Sequence 9, Application US/09832312 | | ; Patent No. US20010049829A1 | |
| ; GENERAL INFORMATION: | | ; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF | |
| ; FILE REFERENCE: 7853-234 | | ; CURRENT APPLICATION NUMBER: US/09/832,312 | |
| ; PRIOR FILING DATE: 2001-04-09 | | ; PRIOR APPLICATION NUMBER: 09/610,118 | |
| ; PRIOR FILING DATE: 2000-06-30 | | ; PRIOR APPLICATION NUMBER: 09/503,387 | |
| ; PRIOR FILING DATE: 2000-02-14 | | ; PRIOR APPLICATION NUMBER: 09/454,824 | |
| ; PRIOR FILING DATE: 1999-12-06 | | ; PRIOR APPLICATION NUMBER: 09/345,468 | |
| ; PRIOR FILING DATE: 1999-06-30 | | ; SOFTWARE: FastSeq for Windows Version 3.0 | |
| ; SEQ ID NO 9 | | ; LENGTH: 249 | |
| ; TYPE: PRT | | ; ORGANISM: Homo sapiens | |
| ; US-09-832-312-9 | | Query Match | |
| | | Best Local Similarity 100.0%; Score 1304; DB 9; Length 249; | |
| | | Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| QY | 1 | QSGPLPKPSIQALPSSLVPLEKPTLRQGP | GVLDYRLEKLSSSRYQQAFLFPAKR 60 |
| DB | 1 | QSGPLPKPSIQALPSSLVPLEKPTLRQGP | GVLDYRLEKLSSSRYQQAFLFPAKR 60 |
| QY | 61 | SLAGRYRCSYONGSLWSLPSDQLELVATGV | FAKPSLSAQPGFAVSSGGVTLQCQTRYGF 120 |
| DB | 61 | SLAGRYRCSYONGSLWSLPSDQLELVATGV | FAKPSLSAQPGFAVSSGGVTLQCQTRYGF 120 |

```
QY 121 DQFALYKEGDPAPYKNPERWRASFPITVTAAHSGTYRCYSFSSSRDPYLSAPSDPLEL 180
      |||||||
Db 121 DQFALYKEGDPAPYKNPERWRASFPITVTAAHSGTYRCYSFSSSRDPYLSAPSDPLEL 180
QY 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFETETSRISITTSPEKSDSPAGP 240
      |||||||
Db 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFETETSRISITTSPEKSDSPAGP 240
QY 241 ARQYTTKGN 249
      |||||||
Db 241 ARQYTTKGN 249

RESULT 2
US-09-832-312-5
; Sequence 5, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-312-5

Query Match 100.0%; Score 1304; DB 9; Length 319;
Best Local Similarity 100.0%; Pred. No. 6.6e-104;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLEKLSRSSRYQDQAVLFIPAKMR 60
      |||||||
Db 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLEKLSRSSRYQDQAVLFIPAKMR 60
QY 61 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQGPAPVSSGGDVTLQCQTRYGF 120
      |||||||
Db 61 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQGPAPVSSGGDVTLQCQTRYGF 120
QY 121 DQFALYKEGDPAPYKNPERWRASFPITVTAAHSGTYRCYSFSSSRDPYLSAPSDPLEL 180
      |||||||
Db 121 DQFALYKEGDPAPYKNPERWRASFPITVTAAHSGTYRCYSFSSSRDPYLSAPSDPLEL 180
QY 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFETETSRISITTSPEKSDSPAGP 240
      |||||||
Db 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFETETSRISITTSPEKSDSPAGP 240
QY 241 ARQYTTKGN 249
      |||||||
Db 241 ARQYTTKGN 249

RESULT 3
US-09-832-312-3
; Sequence 3, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
```

```
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-312-3

Query Match 100.0%; Score 1304; DB 9; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.2e-104;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLEKLSRSSRYQDQAVLFIPAKMR 60
      |||||||
Db 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLEKLSRSSRYQDQAVLFIPAKMR 60
QY 61 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQGPAPVSSGGDVTLQCQTRYGF 120
      |||||||
Db 61 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQGPAPVSSGGDVTLQCQTRYGF 140
QY 121 DQFALYKEGDPAPYKNPERWRASFPITVTAAHSGTYRCYSFSSSRDPYLSAPSDPLEL 180
      |||||||
Db 121 DQFALYKEGDPAPYKNPERWRASFPITVTAAHSGTYRCYSFSSSRDPYLSAPSDPLEL 200
QY 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFETETSRISITTSPEKSDSPAGP 240
      |||||||
Db 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFETETSRISITTSPEKSDSPAGP 260
QY 241 ARQYTTKGN 249
      |||||||
Db 241 ARQYTTKGN 269

RESULT 4
US-10-157-031-387
; Sequence 387, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobachev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequen
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 387
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-157-031-387

Query Match 100.0%; Score 1304; DB 15; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.2e-104;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLEKLSRSSRYQDQAVLFIPAKMR 60
      |||||||
Db 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLEKLSRSSRYQDQAVLFIPAKMR 80
QY 61 SLAGRYRCSYQNGSLWLSLPSDQLELVATGVFAKPSLSAQGPAPVSSGGDVTLQCQTRYGF 120
```

```

      |||
Db      81 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCCTRYGF 140
      |||
Qy      121 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 180
      |||
Db      141 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 200
      |||
Qy      181 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRSITTSPEKESDSPAGP 240
      |||
Db      201 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRSITTSPEKESDSPAGP 260
      |||
Qy      241 ARQYTTKGN 249
      |||
Db      261 ARQYTTKGN 269
```

```

RESULT 5
US-10-446-826-37
; Sequence 37, Application US/10446826
; Publication No. US20030186885A1
; GENERAL INFORMATION:
; APPLICANT: TANDON, NARENDRA N.
; APPLICANT: SUN, BING
; APPLICANT: NAKAMURA, TAKASHI
; APPLICANT: YAMAMOTO, NAOMASA
; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
; FILE REFERENCE: 03459,0026-00000
; CURRENT APPLICATION NUMBER: US/10/446,826
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/653,255B
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: PCT/US00/23975
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-826-37
```

```

Query Match      100.0%; Score 1304; DB 12; Length 369;
Best Local Similarity 100.0%; Pred. No. 8e-104;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGGPPGVDLVRLLEKLSSSRYQDQAVLFIPAMKR 60
      |||
Db      98 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGGPPGVDLVRLLEKLSSSRYQDQAVLFIPAMKR 157
      |||
Qy      61 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCCTRYGF 120
      |||
Db      158 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCCTRYGF 217
      |||
Qy      121 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 180
      |||
Db      219 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 277
      |||
Qy      181 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRSITTSPEKESDSPAGP 240
      |||
Db      278 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRSITTSPEKESDSPAGP 337
      |||
Qy      241 ARQYTTKGN 249
      |||
Db      338 ARQYTTKGN 346
```

RESULT 6
US-09-832-312-34

```

; Sequence 34, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-34
```

```

Query Match      99.7%; Score 1300; DB 9; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.6e-103;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGGPPGVDLVRLLEKLSSSRYQDQAVLFIPAMKR 60
      |||
Db      21 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGGPPGVDLVRLLEKLSSSRYQDQAVLFIPAMKR 80
      |||
Qy      61 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCCTRYGF 120
      |||
Db      81 SLAGRYRCSYQNGSLMSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCCTRYGF 140
      |||
Qy      121 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 180
      |||
Db      141 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 200
      |||
Qy      181 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRSITTSPEKESDSPAGP 240
      |||
Db      201 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRSITTSPEKESDSPAGP 260
      |||
Qy      241 ARQYTTKGN 249
      |||
Db      261 ARQYTTKGN 269
```

```

RESULT 7
US-09-832-312-36
; Sequence 36, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-09-832-312-36

| | | | | |
|-----------------------|--------------|--------------------|--------------|------------|
| Query Match | 99.7% | Score 1300 | DB 9 | Length 339 |
| Best Local Similarity | 99.6% | Pred. No. 1.6e-103 | | |
| Matches 248 | Conservative | 0 | Mismatches 1 | Indels 0 |
| | | | | Gaps 0 |

| | | | | | | |
|----|-----|-----------------------------------|---------------------|-----------|-------------|-----|
| QY | 1 | QSGPLPKPESLQALPSSSLVPLEKPVTLRCQGP | PGVDLRLLEKLTSSSR | YQDQANLFI | PAMKR | 60 |
| Db | 21 | QSGPLPKPESLQALPSSSLVPLEKPVTLRCQGP | PGVDLRLLEKLTSSSR | YQDQVVLFI | PAMKR | 80 |
| QY | 61 | SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAK | ESLSAQPGPAVSSGGDVT | IQCCTR | RYGF | 120 |
| Db | 81 | SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAK | PSLSAQPGPAVSSGGDVT | IQCCTR | RYGF | 140 |
| QY | 121 | DQFALYKESGDPAPYKKNPERMYRASFP | ITVTAHSGTYRCYSFSSRD | PLYMSKAS | PSDPLEL | 180 |
| Db | 141 | DQFALYKESGDPAPYKKNPERMYRASFP | ITVTAHSGTYRCYSFSSRD | PLYMSKAS | PSDPLEL | 200 |
| QY | 181 | VVTGTSVTEPSRLPTEPPSSVAEFSEATAEL | TVSPFNKVFETETGRS | ITTS | SPKESDSPAGP | 240 |
| Db | 201 | VVTGTSVTEPSRLPTEPPSSVAEFSEATAEL | TVSPFNKVFETETGRS | ITTS | SPKESDSPAGP | 260 |
| QY | 241 | ARQYVYTKGN | 249 | | | |
| Db | 261 | ARQYVYTKGN | 269 | | | |

RESULT 8

```

US-09-832-312-38
; Sequence 38, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GYCCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/630,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-38

```

| | | | | |
|-----------------------|--------------|--------------------|--------------|------------|
| Query Match | 99.7% | Score 1300 | DB 9 | Length 339 |
| Best Local Similarity | 99.6% | Pred. No. 1.6e-103 | | |
| Matches 248 | Conservative | 0 | Mismatches 1 | Indels 0 |
| | | | | Gaps 0 |

| | | | |
|----|-----|---|-----|
| QY | 1 | QSGPLPKPSLQALPSSLVLEKEPVTLRCCGPPGVDELRYLEKLSRRYQDDAVLEIPAMKR | 63 |
| Db | 21 | QSGPLPKPSLQALPSSLVLEKEPVTLRCCGPPGVDLRYLEKLSRRYQDDAVLEIPAMKR | 83 |
| QY | 61 | SLAGRYRCSTQNGSLWLSLPSDDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLLQOQTRYGF | 120 |
| Db | 81 | SLAGRYRCSTQNGSLWLSLPSDDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLLQOQTRYGF | 140 |
| QY | 121 | DQFALYKEGDPAFYKNPERWYRASFPITVTAAHSGTRYRCYSFSSRRDPYLMASDPLEL | 180 |
| Db | 141 | DQFALYKEGDPAFYKNPERWYRASFPITVTAAHSGTRYRCYSFSSRRDPYLMASDPLEL | 200 |
| QY | 181 | VVTGTSVTPSRRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRSYTTSPKESDSPAPG | 240 |
| Db | 201 | VVTGTSVTPSRRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRSYTTSPKESDSPAPG | 260 |

| | | | |
|----|-----|-----------|-----|
| 2Y | 241 | ARQYTTKGN | 249 |
| | | | |
| Db | 261 | ARQYTTKGN | 269 |

RESJIT 3

```

US-09-832-312-40
; Sequence 40, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: G2YCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 40
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-832-312-40

```

| | | | | |
|-----------------------|--------------|--------------------|--------------|------------|
| Query Match | 99.7% | Score 1300 | DB 9 | Length 339 |
| Best Local Similarity | 99.6% | Pred. No. 1.6e-103 | | |
| Matches 248 | Conservative | 0 | Mismatches 1 | Indels 0 |
| | | | | Gaps 0 |

| | | | |
|----|-----|--|-----|
| QY | 1 | QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLRYLEKLTSSSRVQDQAVLFIPAYKR | 60 |
| DB | 21 | QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPPGVDLRYLEKLTSSSRVQDQAVLFIPAYKR | 80 |
| QY | 61 | SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGVTLQCCQTRYGF | 120 |
| DB | 81 | SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGVTLQCCQTRYGF | 140 |
| QY | 121 | DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSFSSRDPLYLWSAPSDPTEL | 180 |
| DB | 141 | DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSFSSRDPLYLWSAPSDPTEL | 200 |
| QY | 181 | VVTGTSVTPSRLEPTEPPSSVAEFSSEATAELTVSFNNKVFITEISRSTTSPKESDSPA | 240 |
| DB | 201 | VVTGTSVTPSRLEPTEPPSSVAEFSSEATAELTVSFNNKVFITEISRSTTSPKESDSPA | 260 |
| QY | 241 | AROYTTKGN | 249 |
| DB | 261 | AROYTTKGN | 269 |

RESULT 10

US-10-446-826-5
 ; Sequence 5, Application US/10446826
 ; Publication No. US20030186885A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANDON, NARENDRA N.
 ; APPLICANT: SUN, BING
 ; APPLICANT: YAKAMURA, TAKASHI
 ; APPLICANT: YAMAMOTO, NAOMASA
 ; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
 ; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
 ; FILE REFERENCE: 03459.0026-00000
 ; CURRENT APPLICATION NUMBER: US/10/446,826
 ; CURRENT FILING DATE: 2003-05-29
 ; PRIOR APPLICATION NUMBER: US/09/653,255B
 ; PRIOR FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: PCT/US00/23975

/ PRIOR FILING DATE: 2000-09-01
/ PRIOR APPLICATION NUMBER: 60/152,197
/ PRIOR FILING DATE: 1999-09-01
/ PRIOR APPLICATION NUMBER: 60/158,251
/ PRIOR FILING DATE: 1999-10-08
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 5
/ LENGTH: 339
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-446-826-5

Query Match: 97.9%; Score 1277; DB 12; Length 339;
Best Local Similarity 98.8%; Pred. No. 1,56-101;
Matches 246; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVGVDLYRLKLSRRYQDQAVLFIPAMKR 60
DB 21 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVGVDLYRLKLSRRYQDQAVLFIPAMKR 80
QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYGF 120
DB 81 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKBSLSAQPGPAVSSGGDVTLQCQTRYGF 140
QY 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 180
DB 141 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 200
QY 181 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRITTSPEKSDSPAGP 240
DB 201 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRITTSPEKSDSPAGP 260
QY 241 ARQYTTKGN 249
DB 261 ARQYTTKGN 269

RESULT 11
US-09-832-312-19

/ Sequence 19, Application US/09832312
/ Patent No. US20010049829A1
/ GENERAL INFORMATION:
/ APPLICANT: Busfield et al.
/ TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
/ FILE REFERENCE: 7853-234
/ CURRENT APPLICATION NUMBER: US/09/832,312
/ CURRENT FILING DATE: 2001-04-09
/ PRIOR APPLICATION NUMBER: 09/610,118
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: 09/503,387
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: 09/454,824
/ PRIOR FILING DATE: 1999-12-06
/ PRIOR APPLICATION NUMBER: 09/345,468
/ PRIOR FILING DATE: 1999-06-30
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 19
/ LENGTH: 267
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-832-312-19

Query Match: 68.7%; Score 895.5; DB 9; Length 267;
Best Local Similarity 69.9%; Pred. No. 66-69;
Matches 174; Conservative 18; Mismatches 54; Indels 3; Gaps 1;

QY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVGVDLYRLKLSRRYQDQAVLFIPAMKR 60
DB 22 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVGVDLYRLKLSRRYQDQAVLFIPAMKR 81
QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYGF 120

DB 82 SNAGRYRCSYQNGSHWSLPSDQLELVATGVFAKPSLSAHPPSSAVPQGRDVTLLKQSPYSF 141
QY 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 180
DB 142 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 201
QY 181 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRITTSPEKSDSPAGP 240
DB 202 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRITTSPEKSDSPAGP 268
QY 241 ARQYTTKGN 249
DB 259 ARQYTTKGN 267

RESULT 12
US-09-832-312-18

/ Sequence 18, Application US/09832312
/ Patent No. US20010049829A1
/ GENERAL INFORMATION:
/ APPLICANT: Busfield et al.
/ TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
/ FILE REFERENCE: 7853-234
/ CURRENT APPLICATION NUMBER: US/09/832,312
/ CURRENT FILING DATE: 2001-04-09
/ PRIOR APPLICATION NUMBER: 09/610,118
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: 09/503,387
/ PRIOR FILING DATE: 2000-02-14
/ PRIOR APPLICATION NUMBER: 09/454,824
/ PRIOR FILING DATE: 1999-12-06
/ PRIOR APPLICATION NUMBER: 09/345,468
/ PRIOR FILING DATE: 1999-06-30
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 18
/ LENGTH: 292
/ TYPE: PRT
/ ORGANISM: Mus musculus
US-09-832-312-18

Query Match: 68.7%; Score 895.5; DB 9; Length 292;
Best Local Similarity 69.9%; Pred. No. 67-69;
Matches 174; Conservative 18; Mismatches 54; Indels 3; Gaps 1;

QY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVGVDLYRLKLSRRYQDQAVLFIPAMKR 60
DB 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQGPVGVDLYRLKLSRRYQDQAVLFIPAMKR 60
QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYGF 120
DB 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLQCQTRYGF 120
QY 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 180
DB 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSRDPYLSAPSDPLEL 180
QY 181 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRITTSPEKSDSPAGP 240
DB 181 VVTGTSVTPSRLPTEPPSSVAEFSSEATAELTVSFTNKVFTTETSRITTSPEKSDSPAGP 240
QY 241 ARQYTTKGN 249
DB 241 ARQYTTKGN 249

RESULT 13
US-09-832-312-16

/ Sequence 16, Application US/09832312
/ Patent No. US20010049829A1
/ GENERAL INFORMATION:
/ APPLICANT: Busfield et al.

; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-832-312-16

Query Match 68.7%; Score 895.5; DB 9; Length 313;
Best Local Similarity 69.9%; Pred. No. 7.3e-69;
Matches 174; Conservative 18; Mismatches 54; Indels 3; Gaps 1;

QY 1 QSGPLPKPSLQALPSSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSSRYQDQAVLFIPAMKR 60
D 22 QSGPLPKPSLQALPSSSLVPLEQSVILRCQGPFDVDLYRLEKLPKEXYEDQDFLFPTMER 81
QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQGPFAVSSGGDVTLCQCTRYGF 120
D 82 SNAGRYRCSYQNGSHWSLPSDQLELVATGVYAKPSLSAHPSAVPQGRDVTLLKQSPYSF 141
QY 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRCYSFSSRDPLYMSAPSDPLEL 180
D 142 DEFVLKKEGDTGPKRPEKMYRANFPITVTAHSGTYRCYSFSSSSPYLMSAPSDPLVL 201
QY 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAEITVSTNKVFTTETSRSITTSPEKSDSPAGP 240
D 202 VVTGLSATPSQVPTEESPVTESRRPSILP---TNKISTTEKPMNITASPEGLSPPIGF 258
QY 241 ARQYTTKGN 249
D 259 AHQHYAKGN 267

RESULT 14

US-09-832-312-48
; Sequence 48, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-832-312-48

Query Match 68.7%; Score 895.5; DB 9; Length 313;
Best Local Similarity 69.9%; Pred. No. 7.3e-69;

Matches 174; Conservative 18; Mismatches 54; Indels 3; Gaps 1;
QY 1 QSGPLPKPSLQALPSSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSSRYQDQAVLFIPAMKR 60
D 22 QSGPLPKPSLQALPSSSLVPLEQSVILRCQGPFDVDLYRLEKLPKEXYEDQDFLFPTMER 81
QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQGPFAVSSGGDVTLCQCTRYGF 120
D 82 SNAGRYRCSYQNGSHWSLPSDQLELVATGVYAKPSLSAHPSAVPQGRDVTLLKQSPYSF 141
QY 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRCYSFSSRDPLYMSAPSDPLEL 180
D 142 DEFVLKKEGDTGPKRPEKMYRANFPITVTAHSGTYRCYSFSSSSPYLMSAPSDPLVL 201
QY 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAEITVSTNKVFTTETSRSITTSPEKSDSPAGP 240
D 202 VVTGLSATPSQVPTEESPVTESRRPSILP---TNKISTTEKPMNITASPEGLSPPIGF 258
QY 241 ARQYTTKGN 249
D 259 AHQHYAKGN 267

RESULT 15

US-09-832-312-42
; Sequence 42, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 42
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-832-312-42

Query Match 68.4%; Score 891.5; DB 9; Length 313;
Best Local Similarity 69.5%; Pred. No. 1.6e-68;
Matches 173; Conservative 18; Mismatches 55; Indels 3; Gaps 1;

QY 1 QSGPLPKPSLQALPSSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSSRYQDQAVLFIPAMKR 60
D 22 QSGPLPKPSLQALPSSSLVPLEQSVILRCQGPFDVDLYRLEKLPKEXYEDQDFLFPTMER 81
QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQGPFAVSSGGDVTLCQCTRYGF 120
D 82 SNAGRYRCSYQNGSHWSLPSDQLELVATGVYAKPSLSAHPSAVPQGRDVTLLKQSPYSF 141
QY 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAHSGTYRCYSFSSRDPLYMSAPSDPLEL 180
D 142 DEFVLKKEGDTGPKRPEKMYRANFPITVTAHSGTYRCYSFSSSSPYLMSAPSDPLVL 201
QY 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAEITVSTNKVFTTETSRSITTSPEKSDSPAGP 240
D 202 VVTGLSATPSQVPTEESPVTESRRPSILP---TNKISTTEKPMNITASPEGLSPPIGF 258
QY 241 ARQYTTKGN 249
D 259 AHQHYAKGN 267

Mon Nov 10 06:30:17 2003

us-09-503-387-9.rapb

Page 7

Search completed: November 10, 2003, 06:28:48
Job time : 446 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2003, 06:14:09 ; Search time 41 seconds

(without alignments)
363,974 Million cell updates/sec

Title: US-09-503-387-9

Perfect score: 1304
Sequence: 1 QSGPLPKPSLQALPSSLVPL.....SPKESDSPASPARQYTKGN 249

Scoring table: Biostat62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_19Jul03:*
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.*
12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.*
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT.*
14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID | Description |
|------------|-------|-------------|--------|----|----------|--------------------|
| 1 | 1304 | 100.0 | 249 | 22 | AAB61261 | Human TANGO 268 ex |
| 2 | 1304 | 100.0 | 249 | 24 | ABU11227 | Human TANGO 268 ex |
| 3 | 1304 | 100.0 | 319 | 22 | AAB61257 | Mature human TANGO |
| 4 | 1304 | 100.0 | 319 | 22 | AAB49403 | Human glycoprotein |
| 5 | 1304 | 100.0 | 319 | 24 | ABU11223 | Human TANGO 268 ex |
| 6 | 1304 | 100.0 | 339 | 22 | AAB61255 | Human TANGO 268 pr |
| 7 | 1304 | 100.0 | 339 | 24 | ABU11221 | Human TANGO 268 pr |
| 8 | 1304 | 100.0 | 369 | 22 | AAV72791 | Human GpVI externa |
| 9 | 1304 | 100.0 | 501 | 24 | ABP72518 | Immunoglobulin FC- |

| | | | | | | |
|----|-------|-------|-----|----|----------|--------------------|
| 10 | 1304 | 100.0 | 512 | 24 | ABP72519 | Glycoprotein VI-im |
| 11 | 1300 | 99.7 | 339 | 22 | AAB61273 | Human TANGO 268-re |
| 12 | 1300 | 99.7 | 339 | 22 | AAB61274 | Human TANGO 268-re |
| 13 | 1300 | 99.7 | 339 | 22 | AAB61275 | Human TANGO 268-re |
| 14 | 1300 | 99.7 | 339 | 22 | AAB61276 | Human TANGO 268-re |
| 15 | 1300 | 99.7 | 339 | 24 | ABU11239 | Glycoprotein VI as |
| 16 | 1300 | 99.7 | 339 | 24 | ABU11240 | Glycoprotein VI as |
| 17 | 1300 | 99.7 | 339 | 24 | ABU11241 | Glycoprotein VI as |
| 18 | 1300 | 99.7 | 339 | 24 | ABU11242 | Glycoprotein VI as |
| 19 | 1295 | 99.3 | 339 | 22 | AAB31668 | Amino acid sequenc |
| 20 | 1277 | 97.9 | 339 | 22 | AAV72790 | Human platelet mem |
| 21 | 970 | 74.4 | 203 | 23 | AAO19266 | Human platelet gly |
| 22 | 895.5 | 68.7 | 267 | 22 | AAB61268 | Mouse TANGO 268 ex |
| 23 | 895.5 | 68.7 | 267 | 24 | ABU11234 | Mouse TANGO 268 pr |
| 24 | 895.5 | 68.7 | 292 | 22 | AAB61267 | Mature mouse TANGO |
| 25 | 895.5 | 68.7 | 292 | 24 | ABU11233 | Mouse TANGO 268 pr |
| 26 | 895.5 | 68.7 | 313 | 22 | AAB61265 | Mouse TANGO 268-re |
| 27 | 895.5 | 68.7 | 313 | 22 | AAB61280 | Mouse TANGO 268-re |
| 28 | 895.5 | 68.7 | 313 | 24 | ABU11231 | Mouse TANGO 268 pr |
| 29 | 895.5 | 68.7 | 313 | 24 | ABU11236 | Glycoprotein VI as |
| 30 | 891.5 | 68.4 | 313 | 22 | AAB61277 | Mouse TANGO 268-re |
| 31 | 891.5 | 68.4 | 313 | 22 | AAB61278 | Mouse TANGO 268-re |
| 32 | 891.5 | 68.4 | 313 | 22 | AAB61279 | Mouse TANGO 268-re |
| 33 | 891.5 | 68.4 | 313 | 24 | ABU11243 | Glycoprotein VI as |
| 34 | 891.5 | 68.4 | 313 | 24 | ABU11244 | Glycoprotein VI as |
| 35 | 891.5 | 68.4 | 313 | 24 | ABU11245 | Glycoprotein VI as |
| 36 | 418 | 32.1 | 448 | 19 | AAW82551 | Human LIR-pbm2 pro |
| 37 | 418 | 32.1 | 448 | 19 | AAW53463 | Human gp49 Hm18 po |
| 38 | 418 | 32.1 | 448 | 21 | AAAC4176 | Leukocyte immunogi |
| 39 | 418 | 32.1 | 472 | 19 | AAW69234 | FCR-IV protein seq |
| 40 | 411 | 31.5 | 447 | 24 | ABR39440 | Human GENSER poly |
| 41 | 409.5 | 31.3 | 632 | 24 | ABU12086 | Human NCV27a CG938 |
| 42 | 405.5 | 31.1 | 631 | 24 | ABU11229 | Human monocyte inh |
| 43 | 404.5 | 31.0 | 337 | 24 | ABR41213 | Human DTHP recept |
| 44 | 404.5 | 31.0 | 500 | 22 | ABG10535 | Novel human diagno |
| 45 | 404.5 | 31.0 | 500 | 22 | AAE10579 | Human macrophage-e |

ALIGNMENTS

| | |
|----------|---|
| RESULT 1 | |
| ID | AAB61261 standard; Protein; 249 AA. |
| XX | |
| AC | AAB61261; |
| XX | |
| CT | 04-APR-2001 (first entry) |
| XX | |
| DE | Human TANGO 268 extracellular domain. |
| XX | |
| KW | Human; TANGO 268; cardiant; cerebroprotective; cytosolic; anticoagulant; |
| KW | thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI; |
| KW | platelet membrane glycoprotein receptor; bleeding disorder; |
| KW | blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke; |
| KW | ischaemia; cardiovascular disease; immunological disease; liver disorder; |
| KW | cancer. |
| XX | |
| OS | Homo sapiens. |
| XX | |
| PK | W0203100810-A1. |
| XX | |
| PD | 04-JAN-2001. |
| XX | |
| PF | 30-JUN-2000; 2000WO-US18152. |
| XX | |
| FR | 30-JUN-1999; 99US-0345468. |
| FR | 06-DEC-1999; 99US-0454824. |
| FR | 14-FEB-2000; 2000US-0503387. |
| XX | |
| PA | (MILL-) MILLENNIUM PHARM INC. |
| XX | |
| PI | Busfield SJ, Villedal J, Jandrot-Perrus M, Vairchencker W, Gill DS; |

P1 Qian WD, Kingsbury G;
 XX
 XX WPI, 2001-030877/09.
 XX
 PT New genes encoding human platelet-expressed collagen receptor,
 PT glycoprotein VI, and its modulators, useful for preventing, treating
 PT and diagnosing hemorrhagic disorders, thrombotic diseases and
 PT immunological disorders.
 XX
 PS Disclosure: Page 203-204; 227pp; English.
 XX
 CC The present sequence is given in a specification relating to an isolated
 CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
 CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
 CC and polypeptides and their modulators, e.g. antisense nucleic acids,
 CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders
 CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
 CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
 CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
 CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
 CC infarction), immunological diseases (e.g. platelet disorder) and
 CC embryonic liver disorders. Preferably they are used to prevent acute
 CC cardiac ischaemia following angioplasty and metastatic cancers,
 CC especially of the colon and liver.
 CC
 XX
 XX Sequence 249 AA;
 XX
 SQ
 Query Match: 100.0%; Score 1304; DB 22; Length 249;
 Best Local Similarity 100.0%; Pred. No. 2.3e-105;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QSGPLPKPSIQALPSSJVLPLEKPVTLRCQSPGVLYRLEKSSSRVQDQAVLFIPAMKR 60
 Eb 1 QSGPLPKPSIQALPSSJVLPLEKPVTLRCQSPGVLYRLEKSSSRVQDQAVLFIPAMKR 60
 QY 61 SLAGRYRCRYQNGSLWSJPSDQLELVATGVFAKPSLSAQPSAVSSGGDVTLQCQTRYGF 120
 Db 61 SLAGRYRCRYQNGSLWSJPSDQLELVATGVFAKPSLSAQPSAVSSGGDVTLQCQTRYGF 120
 QY 121 DQFALYKEGDPAPYKMPERWRASPIITVTAHSGTYRCYSPSSRDYLMASPSDPLE 180
 Db 121 DQFALYKEGDPAPYKMPERWRASPIITVTAHSGTYRCYSPSSRDYLMASPSDPLE 180
 QY 181 VVTGTSVTSRSLPTEPPSSVAEFSEATRELTVSFTNKVFTTETSRSTTSKESDSPAGP 240
 Db 181 VVTGTSVTSRSLPTEPPSSVAEFSEATRELTVSFTNKVFTTETSRSTTSKESDSPAGP 240
 QY 241 ARQYVTKGN 249
 Db 241 ARQYVTKGN 249
 RESULT 2
 ABU11227
 ID ABU11227 standard; Peptide; 249 AA.
 XX
 AC ABU11227;
 XX
 DT 06-FEB-2003 (first entry)
 XX
 DE Human TANGO 268 extracellular domain.
 XX
 KW Human; mouse; variable heavy; VH; antigen: cancer;
 KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
 KW TANGO 268; extracellular matrix; collagen; platelet release;
 KW proliferation; migration; embryogenesis; inflammation; thrombosis;
 KW degradation; thrombocytopaenia; antibody; thrombotic disorder;
 KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
 KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
 KW cardiovascular disease; angina pectoris; myocardial infarction;
 KW coronary restenosis; atherosclerosis; immunological disorder;

KW developmental disorder; embryonic disorder; liver disorder;
 KW cerebral vascular disease; venous thromboembolism disease.
 XX
 OS Homo sapiens.
 XX
 PN K0200280368-A1.
 XX
 PD 17-OCT-2002.
 XX
 PF 03-APR-2002; 2002WC-US:1122.
 XX
 PR 03-APR-2001; 2001US-0829495.
 XX
 PA (MILL-) MILLENNium PHARM INC.
 XX
 PI Busfield SJ, Villeval J, Jandrot-Perrus W, Vanhacker W, Gill DS;
 PI Qian WD, Kingsbury G;
 XX
 DR WPI; 2003-058477/05.
 XX
 PT Novel, substantially purified antibody immunospecifically binding to
 PT TANGO 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
 PT
 XX
 PS Disclosure: Page 212-213; 236pp; English.
 XX
 CC This invention relates to a novel purified antibody comprising a
 CC variable heavy (VH) complementarity determining region (CDR1, VH CDR2
 CC or VH CDR3) or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
 CC immunospecifically binding to a TANGO 268 (also referred as glycoprotein
 CC VI (GPVI)) antigen. The antibodies of the invention act to decrease or
 CC block TANGO 268 binding to extracellular matrix components, or as a
 CC collagen or platelet release and aggregation blocker. The antibodies of
 CC the invention are useful for modulating proliferation, migration,
 CC morphology, differentiation and/or function of megakaryocytes and
 CC platelets, including during development e.g. embryogenesis, modulating
 CC leukocyte-platelet and platelet-endothelium interactions in
 CC inflammation and/or thrombosis, and modulating platelet aggregation and
 CC degranulation. They are also useful for modulating disorders associated
 CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
 CC migration, morphology, differentiation and/or function, e.g. bleeding
 CC disorders such as thrombocytopaenia. Other diseases which may be
 CC modulated by these antibodies are thrombotic disorders, cerebral
 CC vascular diseases (e.g. stroke and ischaemia) venous thromboembolism
 CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
 CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
 CC diseases including angina pectoris, myocardial infarction, coronary
 CC restenosis, atherosclerosis, etc); immunological disorders,
 CC developmental disorders, embryonic disorders, liver disorders, cerebral
 CC vascular diseases, venous thromboembolism disease, coronary diseases,
 CC and metastatic cancers. The antibodies of the invention only causes a
 CC transient decrease in platelet counts, platelet aggregation, and/or
 CC platelet activation and so have some advantages over prior art
 CC methods. The present sequence represents a peptide sequence used to
 CC generate the antibodies of the invention.
 XX
 SQ Sequence 249 AA;
 XX
 Query Match: 100.0%; Score 1304; DB 24; Length 249;
 Best Local Similarity 100.0%; Pred. No. 2.3e-105;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QSGPLPKPSIQALPSSJVLPLEKPVTLRCQSPGVLYRLEKSSSRVQDQAVLFIPAMKR 60
 Db 1 QSGPLPKPSIQALPSSJVLPLEKPVTLRCQSPGVLYRLEKSSSRVQDQAVLFIPAMKR 60
 QY 61 SLAGRYRCRYQNGSLWSJPSDQLELVATGVFAKPSLSAQPSAVSSGGDVTLQCQTRYGF 120
 Db 61 SLAGRYRCRYQNGSLWSJPSDQLELVATGVFAKPSLSAQPSAVSSGGDVTLQCQTRYGF 120
 QY 121 DQFALYKEGDPAPYKMPERWRASPIITVTAHSGTYRCYSPSSRDYLMASPSDPLE 180
 Db 121 DQFALYKEGDPAPYKMPERWRASPIITVTAHSGTYRCYSPSSRDYLMASPSDPLE 180

Db 121 DQFALYKEDGDPAPYKNDPERMYRASFPILITVTAHSGTYRCYSFSSRDPYLWMSAPSDPLEJ 180
 QY 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAEELTVSFTNKVFTEETSSITTSPEKESDSPAGP 240
 Db 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAEELTVSFTNKVFTEETSSITTSPEKESDSPAGP 240
 QY 241 ARQYVTKGN 249
 Db 241 ARQYVTKGN 249

RESULT 3

AAB61257
 ID AAB61257 standard; Protein; 319 AA.

XX AAB61257;
 AC
 XX
 DT 04-APR-2001 (first entry)

XX Mature human TANGO 268 protein.

XX Human; TANGO 268; cardiatic; cerebroprotective; cytostatic; anticoagulant;
 KM thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
 KM platelet membrane glycoprotein receptor; bleeding disorder;
 KM blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 KM ischaemia; cardiovascular disease; immunological disease; liver disorder;
 KM cancer.

XX Homo sapiens.

XX NC200100810-A1.

XX 04-JAN-2001.

XX 30-JUN-2000; 2000WO-US18152.

XX 30-JUN-1999; 99US-0345468.

XX 06-DEC-1999; 99US-0454824.

XX 14-FEB-2000; 2000US-0503387.

XX (MILL-) MILLENNIUM PHARM INC.

XX Busfield SJ, Villelaj C, Jandrot-Perrus M, Vainchencker W, Gill ES;
 PI Qian XD, Kingsbury G;

XX WPI; 2001-080877/09.

XX New genes encoding human platelet-expressed collagen receptor,
 PT glycoprotein VI, and its modulators, useful for preventing, treating
 PT and diagnosing hemorrhagic disorders, thrombotic diseases and
 PT immunological disorders -

XX Disclosure; Fig 2; 227pp; English.

XX The present sequence is given in a specification relating to an isolated
 CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
 CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
 CC and polypeptides and their modulators, e.g. antisense nucleic acids,
 CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders
 CC (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
 CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
 CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
 CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
 CC infarction), immunological diseases (e.g. platelet disorder) and
 CC embryonic liver disorders. Preferably they are used to prevent acute
 CC cardiac ischaemia following angioplasty and metastatic cancers,
 CC especially of the colon and liver.

XX Sequence 319 AA;

Query Match

100.0%; Score 1304; DB 22; Length 319;

Best Local Similarity 100.0%; Pred. No. 3.2e-105;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSGLVPLEKPYTRCQGPVGDLVRLLEKLSSRRYQDAVJFPAWKR 60

Db 1 QSGPLPKPSLQALPSGLVPLEKPYTRCQGPVGDLVRLLEKLSSRRYQDAVJFPAWKR 60

QY 61 SLAGRYCSYONGSLMSLPSDQLBLVATGVFAKPSLSAOPGPAVSSGGDVTLOCCOTRYGF 120

Db 61 SLAGRYCSYONGSLMSLPSDQLBLVATGVFAKPSLSAOPGPAVSSGGDVTLOCCOTRYGF 120

QY 121 DQFALYKEDGDPAPYKNDPERMYRASFPILITVTAHSGTYRCYSFSSRDPYLWMSAPSDPLEJ 180

Db 121 DQFALYKEDGDPAPYKNDPERMYRASFPILITVTAHSGTYRCYSFSSRDPYLWMSAPSDPLEJ 180

QY 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAEELTVSFTNKVFTEETSSITTSPEKESDSPAGP 240

Db 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAEELTVSFTNKVFTEETSSITTSPEKESDSPAGP 240

QY 241 ARQYVTKGN 249

Db 241 ARQYVTKGN 249

RESULT 4
 AAB49403
 ID AAB49403 standard; Protein; 319 AA.

XX AAB49403;

XX 05-MAR-2001 (first entry)

XX Human glycoprotein VI mature protein.

XX Human; thrombolytic; cardiatic; glycoprotein VI; GPVI;
 KM platelet membrane glycoprotein; platelet activation;
 KM platelet-collagen interaction; thrombotic disorder;
 KM cardiovascular disorder.

XX Homo sapiens.

XX WO200068377-A1.

XX 16-NOV-2000.

XX 25-APR-2000; 2000WO-EP03683.

XX 07-MAY-1999; 99EP-0109094.

XX (MERE) MERCK PATENT GMBH.

XX Clemenson KJ;

XX WPI; 2001-007394/01.

XX N-PSDB; AAC8398C.

XX Recombinant human glycoprotein VI, useful for treating thrombotic,
 PT cardiovascular diseases or platelet-collagen interactions -

XX Claim 5; Fig 1; 27pp; English.

XX The present sequence is human glycoprotein VI (GPVI) mature protein. GPVI
 CC is a platelet membrane glycoprotein which forms a complex together with
 CC the Fc gamma common subunit, which is critical for platelet activation in
 CC response to collagen. GPVI is useful as a screening tool for detecting
 CC specific inhibitors of platelet-collagen interactions, and as a marker
 CC for platelet age and platelet exposure to thrombotic and cardiovascular
 CC disorders. GPVI is also useful for the manufacture of medicaments in the
 CC therapeutic field of thrombotic and cardiovascular events, and disorders
 CC related to platelet-collagen interactions.

XX Sequence 319 AA;

```
Query Match      100.0%; Score 1304; DB 22; Length 319;
Best Local Similarity 100.0%; Pred. No. 3.2e-105;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSSLVPLEKPVTLRCQGPVGVDLYRLEKLSSSRRYQDQAVLFIPAMKR 60
Db 1 QSGPLPKPSLQALPSSSLVPLEKPVTLRCQGPVGVDLYRLEKLSSSRRYQDQAVLFIPAMKR 60
QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYGF 120
Db 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYGF 120
QY 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSSRDYLMASAPSDPLEL 180
Db 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSSRDYLMASAPSDPLEL 180
QY 181 VWTGTSVTPSRLPTEPPSSVAEFSEATAEITVSFTNKVFETTSRSITTSPKESDSPAGP 240
Db 181 VWTGTSVTPSRLPTEPPSSVAEFSEATAEITVSFTNKVFETTSRSITTSPKESDSPAGP 240
QY 241 ARQYTTKGN 249
Db 241 ARQYTTKGN 249

RESULT 5
ABU11223
ID ABU11223 standard; Protein; 319 AA.
XX AC ABU11223;
XX DT 06-FEB-2003 (first entry)
XX DE Human TANGO 268 mature protein.
XX KW Human; mouse; variable heavy; VH; antigen; cancer;
XX KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
XX KW TANGO 268; extracellular matrix; collagen; platelet release;
XX KW proliferation; migration; embryogenesis; inflammation; thrombosis;
XX KW degeneration; thrombocytopaenia; antibody; thrombotic disorder;
XX KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
XX KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
XX KW cardiovascular disease; angina pectoris; myocardial infarction;
XX KW coronary restenosis; atherosclerosis; immunological disorder;
XX KW developmental disorder; embryonic disorder; liver disorder;
XX KW cerebral vascular disease; venous thromboembolism disease.
XX OS Homo sapiens.
XX PN WC200280968-A1.
XX PD 17-OCT-2002.
XX PF 09-APR-2002; 2002WO-US11122.
XX PR 09-APR-2001; 2001US-0829495.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Busfield SJ, Villerval J, Candrot-Perrus M, Vainchencker W, Gill DS,
XX PI Qian DM, Kingsbury G;
XX DR WPI; 2003-058477/05.
XX PT Novel substantially purified antibody immunospecifically binding to
XX PT TANGO 268 antigen, useful for treating bleeding disorders such as
XX PT thrombocytopaenia, stroke, ischaemia, pulmonary embolism, atherosclerosis
XX PS Disclosure; Page 211-212; 236pp; English.
XX CC This invention relates to a novel purified antibody comprising a
XX CC variable heavy (VH) complementarity determining region (CDR)1, VH CDR2
```

```
CC or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
CC immunospecifically binding to a TANGO 268 (also referred as glycoprotein
CC VI (GPVI)) antigen. The antibodies of the invention act to decrease or
CC block TANGO 268 binding to extracellular matrix components, or as a
CC collagen or platelet release and aggregation blocker. The antibodies of
CC the invention are useful for modulating proliferation, migration,
CC morphology, differentiation and/or function of megakaryocytes and
CC platelets, including during development e.g. embryogenesis, modulating
CC leukocyte-platelet and platelet-endothelium interactions in
CC inflammation and/or thrombosis, and modulating platelet aggregation and
CC degranulation. They are also useful for modulating disorders associated
CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
CC migration, morphology, differentiation and/or function, e.g. bleeding
CC disorders such as thrombocytopaenia. Other diseases which may be
CC modulated by these antibodies are thrombotic disorders, cerebral
CC vascular diseases (e.g. stroke and ischaemia) venous thromboembolism
CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
CC diseases including angina pectoris, myocardial infarction, coronary
CC restenosis, atherosclerosis, etc); immunological disorders,
CC developmental disorders, embryonic disorders, liver disorders, cerebral
CC vascular diseases, venous thromboembolism disease, coronary diseases,
CC and metastatic cancers. The antibodies of the invention only causes a
CC transient decrease in platelet counts, platelet aggregation, and/or
CC platelet activation and so have some advantages over prior art
CC methods. The present sequence represents a protein sequence used to
CC create the antibodies of the invention.
XX SQ Sequence 319 AA;

Query Match      100.0%; Score 1304; DB 24; Length 319;
Best Local Similarity 100.0%; Pred. No. 3.2e-105;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSSLVPLEKPVTLRCQGPVGVDLYRLEKLSSSRRYQDQAVLFIPAMKR 60
Db 1 QSGPLPKPSLQALPSSSLVPLEKPVTLRCQGPVGVDLYRLEKLSSSRRYQDQAVLFIPAMKR 60
QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYGF 120
Db 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCQCTRYGF 120
QY 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSSRDYLMASAPSDPLEL 180
Db 121 DQFALYKEGDPAPYKNPERWYRASFPITVTAAHSGTYRCYSSSSRDYLMASAPSDPLEL 180
QY 181 VWTGTSVTPSRLPTEPPSSVAEFSEATAEITVSFTNKVFETTSRSITTSPKESDSPAGP 240
Db 181 VWTGTSVTPSRLPTEPPSSVAEFSEATAEITVSFTNKVFETTSRSITTSPKESDSPAGP 240
QY 241 ARQYTTKGN 249
Db 241 ARQYTTKGN 249

RESULT 6
AAB61255
ID AAB61255 standard; Protein; 339 AA.
XX AC AAB61255;
XX DT 04-APR-2001 (first entry)
XX DE Human TANGO 268 protein.
XX KW Human; mouse; variable heavy; VH; antigen; cancer;
XX KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
XX KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
XX KW platelet membrane glycoprotein receptor; bleeding disorder;
XX KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
XX KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
XX KW cancer.
XX OS Homo sapiens.
```

XX
PN WO200100810-A1.
XX
PD 04-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US18152.
XX
PR 30-JUN-1999; 99US-0345468.
PR 06-DEC-1999; 99US-0454824.
PR 14-FEB-2000; 2000US-0503387.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ, Vilelaval C, Jandrot-Perrus W, Vainchencker W, Gili DS;
PI Qian DM, Kingsbury G;
XX
DR WPI, 2001-080877/09.
DR N-PSDB; AAF29470, AAF29471.
XX
PT New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders -
XX
PS Claim 8; Fig 1A; 227pp; English.
XX
CC The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorders) and
CC embryonic liver disorders. Preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers.
CC
XX
SQ Sequence 339 AA;
XX
Query Match 100.0%; Score 1304; DB 22; Length 339;
Best Local Similarity 100.0%; Pred. No. 3.5e-105;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QSGPLPKPSLQALPSSSLVPLEKPTLRCQGGVGLYRLLEKLSSSRYPQDAVLFIPAMKR 60
DB 21 QSGPLPKPSLQALPSSSLVPLEKPTLRCQGGVGLYRLLEKLSSSRYPQDAVLFIPAMKR 83
QY 61 SLAGRYRCYQNGSJWSLPSDQJELVATGVFAKPSLSAQPGPAVSSGGCVTLQCCQTRYGF 120
DB 81 SLAGRYRCYQNGSJWSLPSDQJELVATGVFAKPSLSAQPGPAVSSGGCVTLQCCQTRYGF 140
QY 121 DCFALYKEGDPAPYKMPERWYRASFPITVTAAHSGTYRCYSSSRDPYJMSAPDPEJ 180
DB 141 DCFALYKEGDPAPYKMPERWYRASFPITVTAAHSGTYRCYSSSRDPYJMSAPDPEJ 200
QY 181 VWTGTSVPSRLPTEPPSSVAEFSSEATAEITVSTFNKYFTTETSRSITTSPEKESDAP 240
DB 201 VWTGTSVPSRLPTEPPSSVAEFSSEATAEITVSTFNKYFTTETSRSITTSPEKESDAP 260
QY 241 ARQYTTKGN 249
DB 261 ARQYTTKGN 269
RESULT 7
ABU11221
ID ABU11221 standard; Protein: 339 AA.
XX

AC ABU11221;
XX
DT 06-FEB-2003 (first entry)
XX
DE Human TANGO 268 protein.
XX
KW Human; mouse; variable heavy; VH; antigen; cancer;
KW complementarity determining region; TANGO 268; glycoprotein VI; GPVI;
KW TANGO 268; extracellular matrix; collagen; platelet release;
KW proliferation; migration; embryogenesis; inflammation; thrombosis;
KW degeneration; thrombocytopaenia; antibody; thrombotic disorder;
KW cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
KW leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
KW cardiovascular disease; angina pectoris; myocardial infarction;
KW coronary stenosis; atherosclerosis; immunological disorder;
KW developmental disorder; embryonic disorder; liver disorder;
KW cerebral vascular disease; venous thromboembolism disease.
XX
OS Homo sapiens.
XX
PN WO2002050368-A1.
XX
PD 17-OCT-2002.
XX
PF 09-APR-2002; 2002WO-US11122.
XX
PR 09-APR-2001; 2001US-0829495.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SJ, Vilelaval C, Jandrot-Perrus W, Vainchencker W, Gili DS;
PI Qian DM, Kingsbury G;
XX
DR WPI; 2003-058477/05.
DR N-PSDB; ABX17291, ABX17290.
XX
PT Novel substantially purified antibody immunospecifically binding to
PT TANGO 268 antigen, useful for treating bleeding disorders such as
PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
PT
XX
PS Disclosure; Figure 1; 236pp; English.
XX
CC This invention relates to a novel purified antibody comprising a
CC variable heavy (VH) complementarity determining region (CDR)1, VH CDR2
CC or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
CC immunospecifically binding to a TANGO 268 (also referred as glycoprotein
CC VI (GPVI)) antigen. The antibodies of the invention act to decrease or
CC block TANGO 268 binding to extracellular matrix components, or as a
CC collagen or platelet release and aggregation blocker. The antibodies of
CC the invention are useful for modulating proliferation, migration,
CC morphology, differentiation and/or function of megakaryocytes and
CC platelets, including during development e.g. embryogenesis, modulating
CC leukocyte-platelet and platelet-endothelium interactions in
CC inflammation and/or thrombosis, and modulating platelet aggregation and
CC degranulation. They are also useful for modulating disorders associated
CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
CC migration, morphology, differentiation and/or function, e.g. bleeding
CC disorders such as thrombocytopaenia. Other diseases which may be
CC modulated by these antibodies are thrombotic disorders, cerebral
CC vascular diseases (e.g. stroke and ischaemia) venous thromboembolism
CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
CC diseases including angina pectoris, myocardial infarction, coronary
CC stenosis, atherosclerosis, etc); immunological disorders,
CC developmental disorders, embryonic disorders, liver disorders, cerebral
CC vascular diseases, venous thromboembolism disease, coronary diseases,
CC and metastatic cancers. The antibodies of the invention only causes a
CC transient decrease in platelet counts, platelet aggregation, and/or
CC platelet activation and so have some advantages over prior art
CC methods. The present sequence represents a protein sequence used to
CC create the antibodies of the invention.
XX

SQ Sequence 339 AA;
 Query Match 100.0%; Score 1304; DB 24; Length 339;
 Best Local Similarity 100.0%; Pred. No. 3,5e-105;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQPPGVLDYRLKLSRRYQDQAVLFIPAMKR 60
 |||||
 DB 21 QSGPLPKPSLQALPSSLVPLEKPYTLRCQPPGVLDYRLKLSRRYQDQAVLFIPAMKR 80
 QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLOCCQTRYGF 120
 |||||
 DB 81 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLOCCQTRYGF 140
 QY 121 DQFALYKEGDPAPYKXNPERWYRASFPITVTAHSGTYRCYSFSSSRDPYLSAPSDPLEL 180
 |||||
 DB 141 DQFALYKEGDPAPYKXNPERWYRASFPITVTAHSGTYRCYSFSSSRDPYLSAPSDPLEL 200
 QY 181 VWTGTSVTPSRLPTEPPSSVAEFSATAELTVSFTNKVFTTETSRSITTSPKESDSPAGP 240
 |||||
 DB 201 VWTGTSVTPSRLPTEPPSSVAEFSATAELTVSFTNKVFTTETSRSITTSPKESDSPAGP 260
 QY 241 ARQYTTKGN 249
 |||||
 DB 261 ARQYTTKGN 269
 RESULT 8
 AAY72791
 ID AAY72791 standard; Protein; 369 AA.
 XX AC AAY72791;
 XX DT 31-MAY-2001 (first entry)
 DE Human GPVI external domain-yeast alpha factor chimera.
 XX KW Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
 XX KM vascular disease; thrombosis; plasmid pPICZGPVI; chimeric protein.
 OS Chimeric - Saccharomyces cerevisiae.
 OS Chimeric - Homo sapiens.
 FH Key location/Qualifiers
 FT Region 98..346 /label= Human_GPVI_external_domain
 FT /note= "Corresponds to 21-269 residues of human
 GPVI protein (AAY72791)"
 FT Region 347..363 /label= Myc_epitope
 FT Region 364..369 /label= His_tag
 PN WO200116321-A1.
 XX PD 08-MAR-2001.
 XX PF 01-SEP-2000; 2000WO-US23975.
 XX PR 01-SEP-1999; 99US-0152197.
 XX PR 08-OCT-1999; 99US-0158251.
 PA (SUKA) OTSUKA PHARM CO LTD.
 PI Tandon N, Sun B, Nakamura T, Yamamoto N;
 XX WPI; 2001-226691/23.
 DR N-PSDB; AAD02860.
 XX PT Anti-thrombotic medicament, comprising a polypeptide having the
 PT extracellular domain of platelet membrane glycoprotein VI or its
 PT variant, useful for treating a vascular disease and reducing platelet
 PT activation -

XX XX Disclosure; Fig 5; 74pp; English.
 XX The present sequence is a chimeric protein encoded by pPICZGPVI
 CC DNA. The pPICZGPVI encodes human platelet membrane glycoprotein VI
 CC (GPVI) external domain, a yeast alpha-factor, myc epitope and a
 CC histidine (his) tag. The pPICZGPVI is used to produce a soluble
 CC recombinant (sr) GPVI. The medicament comprising GPVI is useful for
 CC treating vascular disease, and for reducing platelet activation which
 CC involves contacting platelets with the medicament. The extracellular
 CC portion of GPVI is used therapeutically to attenuate platelet activation
 CC and aggregation and to treat thrombosis and other vascular diseases.
 CC Antibodies generated against GPVI are used as research and
 CC immunotherapeutic agents.
 SQ Sequence 369 AA;
 Query Match 100.0%; Score 1304; DB 22; Length 369;
 Best Local Similarity 100.0%; Pred. No. 3,9e-105;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QSGPLPKPSLQALPSSLVPLEKPYTLRCQPPGVLDYRLKLSRRYQDQAVLFIPAMKR 60
 |||||
 DB 98 QSGPLPKPSLQALPSSLVPLEKPYTLRCQPPGVLDYRLKLSRRYQDQAVLFIPAMKR 157
 QY 61 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLOCCQTRYGF 120
 |||||
 DB 158 SLAGRYRCSYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLOCCQTRYGF 217
 QY 121 DQFALYKEGDPAPYKXNPERWYRASFPITVTAHSGTYRCYSFSSSRDPYLSAPSDPLEL 180
 |||||
 DB 218 DQFALYKEGDPAPYKXNPERWYRASFPITVTAHSGTYRCYSFSSSRDPYLSAPSDPLEL 277
 QY 181 VWTGTSVTPSRLPTEPPSSVAEFSATAELTVSFTNKVFTTETSRSITTSPKESDSPAGP 240
 |||||
 DB 278 VWTGTSVTPSRLPTEPPSSVAEFSATAELTVSFTNKVFTTETSRSITTSPKESDSPAGP 337
 QY 241 ARQYTTKGN 249
 |||||
 DB 339 ARQYTTKGN 346
 RESULT 9
 ABP72518
 ID ABP72518 standard; Protein; 501 AA.
 XX AC ABP72518;
 XX DT 23-MAY-2003 (first entry)
 DE Immunoglobulin Fc-glycoprotein VI fusion protein.
 XX KW Glycoprotein VI; GPVI; thrombolytic; anticoagulant; antiangiinal;
 XX KW cardiovascular; platelet; collagen; immunoglobulin; antibody;
 XX KW human; mouse; murine; drug screening; nonadhesive; surface coating.
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.
 CS Synthetic.
 FH Key location/Qualifiers
 FT Peptide 1..21 /label= Mouse_antibody_signal_peptide
 FT Protein 22..501 /label= Mature_protein
 FT Region 22..249 /label= Fc
 FT Region 250..252 /label= Linker
 FT Region 253..501 /label= Glycoprotein_VI
 PN WO2003008454-A2.

```
XX 30-JAN-2003.
XX
XX 12-JUL-2002; 2002WO-EP07796.
XX
XX 18-JUL-2001; 2001EP-0116717.
XX
XX (MERE ) MERCK PATENT GMBH.
XX
XX Burger C, Gleitz J, Frech M;
XX
XX WPI; 2003-229561/22.
XX
XX New Glycoprotein VI (GPVI) fusion protein for preventing or treating
XX thrombotic or cardiovascular disorders, comprises a tag molecule and a
XX non-immunoglobulin molecule, e.g. protein or oligopeptide with
XX biological activity of GPVI
XX
XX Claim 9; Page 19-21; 42pp; English.
XX
XX The present sequence is that of a fusion protein comprising an
XX immunoglobulin Fc portion joined via a tripeptide linker to
XX glycoprotein VI (GPVI). The fusion protein includes a mouse antibody
XX N-terminal signal peptide. GPVI is a major platelet glycoprotein
XX which forms a complex with the Fc-gamma common subunit. The GPVI
XX subunit contains a collagen binding site and the Fc-gamma subunit is
XX responsible for signalling. The present Fc-GPVI fusion protein can
XX be obtained by recombinant DNA methods, and is an example of fusion
XX proteins of the invention in which GPVI is linked to a tag such as
XX myc, GST, HA, FLAG, STREP or, preferably, the Fc portion of an
XX immunoglobulin. Such fusion proteins can be used to screen for
XX agonists or antagonists of GPVI-collagen and/or platelet-collagen
XX interactions, and for the treatment of thrombotic and cardiovascular
XX events and disorders related to GPVI-collagen and/or platelet-collagen
XX interactions including increased platelet activation with collagen,
XX atherosclerotic plaque rupture, unstable angina or during surgical
XX treatment such as percutaneous transluminal coronary angioplasty
XX (claimed). The fusion proteins are also useful for coating
XX artificial surfaces to render them nonadhesive for cells, for
XX modifying intraocular lenses to lessen the thrombogenicity of the
XX lens material, for contacting the lens surface, and for covalent
XX crosslinking to modify the lens material (all claimed).
XX
XX Sequence 501 AA;
XX
XX Query Match 100.0%; Score 1304; DB 24; Length 501;
XX Best Local Similarity 100.0%; Pred. No. 5.9e-105;
XX Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 QSGPLPKPSIQALPSSLVLEKPVTLRCGGPGVDLYRLEKLTSSSRVDDQAVLFIPAMKR 60
DB |||||
DB 253 QSGPLPKPSIQALPSSLVLEKPVTLRCGGPGVDLYRLEKLTSSSRVDDQAVLFIPAMKR 312
QY 61 SLAGRYRCGYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLOCGTRRYGF 120
DB |||||
DB 313 SLAGRYRCGYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLOCGTRRYGF 372
QY 121 DQFALYKEGDPAPYKNPBWYRASFPITVTAAHSGTYRCYSSSRDPYLMASPDDEL 180
DB |||||
DB 373 DQFALYKEGDPAPYKNPBWYRASFPITVTAAHSGTYRCYSSSRDPYLMASPDDEL 432
QY 181 VWTGTSVTPSRILPTPESSVAEFSEATAELTVSFTNKVFTTETSRSITSPKESDSDPAGP 240
DB |||||
DB 433 VWTGTSVTPSRILPTPESSVAEFSEATAELTVSFTNKVFTTETSRSITSPKESDSDPAGP 492
QY 241 ARQYTTKGN 249
DB |||||
DB 493 ARQYTTKGN 501
XX
XX RESULT 10
XX ABP72519
XX ID ABP72519 standard; Protein; 512 AA.
```

```
XX AC ABP72519;
XX XX
XX DT 23-MAY-2003 (first entry)
XX
XX DE Glycoprotein VI-immunoglobulin Fc fusion protein.
XX
XX KW Glycoprotein VI; GPVI; thrombolytic; anticoagulant; antianginal;
XX KW cardiovascular; platelet; collagen; immunoglobulin; antibody;
XX KW human; drug screening; nonadhesive; surface coating.
XX
XX OS Homo sapiens.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FH Peptide 1..25
XX FT /label= Oncostatin_M_signal_peptide
XX FT Protein 26..512
XX FT /label= Mature_protein
XX FT Region 26..32
XX FT /label= Linker
XX FT Region 33..281
XX FT /label= Fc
XX FT Region 282..284
XX FT /label= Linker
XX FT Region 285..512
XX FT /label= Glycoprotein_VI
XX
XX PN WO2003008454-A2.
XX
XX PD 30-JAN-2003.
XX
XX PF 12-JUL-2002; 2002WO-EP07796.
XX
XX PR 18-JUL-2001; 2001EP-0116717.
XX
XX PA (MERE ) MERCK PATENT GMBH.
XX
XX PI Burger C, Gleitz J, Frech M;
XX
XX DR WPI; 2003-229561/22.
XX
XX PT New Glycoprotein VI (GPVI) fusion protein for preventing or treating
XX PT thrombotic or cardiovascular disorders, comprises a tag molecule and a
XX PT non-immunoglobulin molecule, e.g. protein or oligopeptide with
XX PT biological activity of GPVI
XX
XX PS Claim 9; Page 21-23; 42pp; English.
XX
XX The present sequence is that of a fusion protein comprising
XX glycoprotein VI (GPVI) joined via a tripeptide linker to the Fc
XX portion of immunoglobulin. The fusion protein includes a human
XX oncostatin M N-terminal signal peptide. GPVI is a major platelet
XX glycoprotein which forms a complex with the Fc-gamma common subunit.
XX The GPVI subunit contains a collagen binding site and the Fc-gamma
XX subunit is responsible for signalling. The present Fc-GPVI fusion
XX protein can be obtained by recombinant DNA methods, and is an example
XX of fusion proteins of the invention in which GPVI is linked to a tag
XX such as myc, GST, HA, FLAG, STREP or, preferably, the Fc portion of
XX an immunoglobulin. Such fusion proteins can be used to screen for
XX agonists or antagonists of GPVI-collagen and/or platelet-collagen
XX interactions, and for the treatment of thrombotic and cardiovascular
XX events and disorders related to GPVI-collagen and/or platelet-collagen
XX interactions including increased platelet activation with collagen,
XX atherosclerotic plaque rupture, unstable angina or during surgical
XX treatment such as percutaneous transluminal coronary angioplasty
XX (claimed). The fusion proteins are also useful for coating
XX artificial surfaces to render them nonadhesive for cells, for
XX modifying intraocular lenses to lessen the thrombogenicity of the
XX lens material, for contacting the lens surface, and for covalent
XX crosslinking to modify the lens material (all claimed).
XX
XX Sequence 512 AA;
```


Query Match 100.0%; Score 1304; DB 24; Length 512;
 Best Local Similarity 100.0%; Pred. No. 6e-105;
 Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSRSSRYQDQAVLFIPAMKR 60
 DB 33 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSRSSRYQDQAVLFIPAMKR 92
 QY 61 SLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLLQCTRIGF 120
 DB 93 SLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLLQCTRIGF 152
 QY 121 DQFALYKEGDPAPYKNPERMYRASFPITVTAAHSGTYRCYSFSSRDPYLMASPSDPLEJ 180
 DB 153 DQFALYKEGDPAPYKNPERMYRASFPITVTAAHSGTYRCYSFSSRDPYLMASPSDPLEJ 212
 QY 181 VWTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTEITSRSITTSPEKSDSPAGP 240
 DB 213 VWTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTEITSRSITTSPEKSDSPAGP 272
 QY 241 ARQYTTKGN 249
 DB 273 ARQYTTKGN 281

RESULT 11
 AAB61273
 ID AAB61273 standard; Protein; 339 AA.
 XX
 AC AAB61273;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human TANGO 268-related protein #1.
 XX
 KW Human; TANGO 268; cardiact; cerebroprotective; cyostatic; anticoagulant;
 KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
 KW platelet membrane glycoprotein receptor; bleeding disorder;
 KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN W0200100810-A1.
 XX
 DT 04-JAN-2001.
 XX
 DE Human TANGO 268-related protein #2.
 XX
 PF 30-JUN-2000; 2000WO-US18152.
 XX
 PR 30-JUN-1999; 99US-0345468.
 PR 06-DEC-1999; 99US-0454824.
 PR 14-FEB-2000; 2000US-0503387.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Busfield SJ, Vileljal J, Jandrot-Perrus M, Vainchencker W, Gill DS;
 PI Qian MD, Kingsbury G;
 XX
 DR WPI; 2001-080877/39.
 DR N-PSDB; AAF29484.
 XX
 PT New genes encoding human platelet-expressed collagen receptor,
 PT glycoprotein VI, and its modulators, useful for preventing, treating
 PT and diagnosing hemorrhagic disorders, thrombotic diseases and
 PT immunological disorders
 XX
 PS Disclosure; Page 213-214; 227pp; English.
 XX
 CC The present sequence is given in a specification relating to an isolated
 CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
 CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides

CC and polypeptides and their modulators, e.g. antisense nucleic acids,
 CC ribozymes and antibodies, are useful for preventing, treating and
 CC diagnosing disorders associated with aberrant expression or activity of
 CC GPVI. These disorders include bleeding disorders
 CC (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
 CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
 CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
 CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
 CC infarction), immunological diseases (e.g. platelet disorder) and
 CC embryonic liver disorders. Preferably they are used to prevent, acture
 CC cardiac ischaemia following angioplasty and metastatic cancers,
 CC especially of the colon and liver.
 XX
 SQ Sequence 339 AA;

Query Match 99.7%; Score 1300; DB 22; Length 339;
 Best Local Similarity 99.6%; Pred. No. 7.8e-105;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSRSSRYQDQAVLFIPAMKR 60
 DB 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSRSSRYQDQAVLFIPAMKR 80
 QY 61 SLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLLQCTRIGF 120
 DB 81 SLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLLQCTRIGF 140
 QY 121 DQFALYKEGDPAPYKNPERMYRASFPITVTAAHSGTYRCYSFSSRDPYLMASPSDPLEJ 180
 DB 141 DQFALYKEGDPAPYKNPERMYRASFPITVTAAHSGTYRCYSFSSRDPYLMASPSDPLEJ 200
 QY 181 VWTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTEITSRSITTSPEKSDSPAGP 240
 DB 201 VWTGTSVTPSRLPTEPPSSVAEFSEATAELTVSFTNKVFTEITSRSITTSPEKSDSPAGP 260
 QY 241 ARQYTTKGN 249
 DB 261 ARQYTTKGN 269

RESULT 12
 AAB61274
 ID AAB61274 standard; Protein; 339 AA.
 XX
 AC AAB61274;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human TANGO 268-related protein #2.
 XX
 KW Human; TANGO 268; cardiact; cerebroprotective; cyostatic; anticoagulant;
 KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
 KW platelet membrane glycoprotein receptor; bleeding disorder;
 KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PN W0200100810-A1.
 XX
 DT 04-JAN-2001.
 XX
 DE Human TANGO 268-related protein #2.
 XX
 PF 30-JUN-2000; 2000WO-US18152.
 XX
 PR 30-JUN-1999; 99US-0345468.
 PR 06-DEC-1999; 99US-0454824.
 PR 14-FEB-2000; 2000US-0503387.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Busfield SJ, Vileljal J, Jandrot-Perrus M, Vainchencker W, Gill DS;
 PI Qian MD, Kingsbury G;

XX WPI: 2001-080877/09.
DR N-PSDB; AAF29485.
XX
PT New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders -
XX
PS Disclosure: Page 214-215; 227pp; English.
XX
CC The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
SQ Sequence 339 AA;
Query Match 99.7%; Score 1300; DB 22; Length 339;
Best Local Similarity 99.6%; Pred. No. 7.8e-105;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSSRYQDQAVLFIPAMKR 60
DB 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSSRYQDQAVLFIPAMKR 80
QY 61 SLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLLQCQTRYGF 120
DB 61 SLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLLQCQTRYGF 140
QY 121 DOFALYXEGDPAPYKNERWYRASFPITVTAAHSGTYRCYSFSSRDPLYLMSAPSDLEL 180
DB 141 DOFALYXEGDPAPYKNERWYRASFPITVTAAHSGTYRCYSFSSRDPLYLMSAPSDLEL 200
QY 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAEITVSFTNKVFTTETSRSITTSFKESDSPAGP 240
DB 201 VVTGTSVTPSRLPTEPPSSVAEFSEATAEITVSFTNKVFTTETSRSITTSFKESDSPAGP 260
QY 241 ARQYTTKGN 249
DB 261 ARQYTTKGN 269
RESULT 13
AAB61275
ID AAB61275 standard; Protein, 339 AA.
XX
AC AAB61275;
XX
XT 04-APR-2001 (first entry)
XX
DE Human TANGO 268-related protein #3.
XX
KW Human, TANGO 268, cardiant, cerebroprotective; cytostatic; anticoagulant;
KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
KW platelet membrane glycoprotein receptor; bleeding disorder;
KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
KW cancer.
XX
OS Homo sapiens.
XX

PN W0200100810-A1.
XX
PD 04-JAN-2001.
XX
PF 30-JUN-2000; 2000WO-US:8152.
XX
PR 30-JUN-1999; 99US-0345468.
PR 06-DEC-1999; 99US-0454624.
PR 14-FEB-2000; 2000US-0503387.
XX
PA (MILL-) MILLENNIUM PHARM INC.
XX
PI Busfield SC, Villedal J, Tandrot-Perrus M, Vainchenker W, Gill DS;
PI Qian MD, Kingsbury G;
XX
DR WPI: 2001-080877/09.
DR N-PSDB; AAF29486.
XX
PT New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders -
XX
PS Disclosure: Page 216; 227pp; English.
XX
CC The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPVI. These disorders include bleeding disorders
CC (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
SQ Sequence 339 AA;
Query Match 99.7%; Score 1300; DB 22; Length 339;
Best Local Similarity 99.6%; Pred. No. 7.8e-105;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSSRYQDQAVLFIPAMKR 60
DB 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSSRYQDQAVLFIPAMKR 80
QY 61 SLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLLQCQTRYGF 120
DB 61 SLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLLQCQTRYGF 140
QY 121 DOFALYXEGDPAPYKNERWYRASFPITVTAAHSGTYRCYSFSSRDPLYLMSAPSDLEL 180
DB 141 DOFALYXEGDPAPYKNERWYRASFPITVTAAHSGTYRCYSFSSRDPLYLMSAPSDLEL 200
QY 181 VVTGTSVTPSRLPTEPPSSVAEFSEATAEITVSFTNKVFTTETSRSITTSFKESDSPAGP 240
DB 201 VVTGTSVTPSRLPTEPPSSVAEFSEATAEITVSFTNKVFTTETSRSITTSFKESDSPAGP 260
QY 241 ARQYTTKGN 249
DB 261 ARQYTTKGN 269
RESULT 14
AAB61276
ID AAB61276 standard; Protein, 339 AA.
XX
AC AAB61276;

XX 04-APR-2001 (first entry)
DT
XX
XX Human TANGO 268-related protein #4.
DE
XX
XX Human; TANGO 268; cardiant; cerebroprotective; cybostatic; anticoagulant;
KM thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPIIb/IIIa;
KM platelet membrane glycoprotein receptor; bleeding disorder;
KM blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
KM ischaemia; cardiovascular disease; immunological disease; liver disorder;
KM cancer.
XX
XX Homo sapiens.
OS
XX WO200100810-A1.
PN
XX 04-JAN-2001.
PD
XX 30-JUN-2000; 2000WO-US18152.
PF
XX 30-JUN-1999; 99US-0345468.
PR 06-DEC-1999; 99US-0454824.
PR 14-FEB-2000; 2000US-0503387.
XX
XX (MIL-) MILLENNIUM PHARM INC.
PA
XX Busfield SJ, Villalal C, Jandrot-Perrus M, Vainchencker W, Gill DS;
PI Qian DM, Kingsbury G;
PI
XX WPI; 2001-080877/09.
DR N-PSDB; AAF29487.
DR
XX
XX New genes encoding human platelet-expressed collagen receptor,
PT glycoprotein VI, and its modulators, useful for preventing, treating
PT and diagnosing hemorrhagic disorders, thrombotic diseases and
PT immunological disorders -
PT
XX
XX Disclosure; Page 217; 227pp; English.
PS
XX
XX The present sequence is given in a specification relating to an isolated
CC nucleic acid molecule encoding a platelet membrane glycoprotein receptor
CC glycoprotein VI (GPIIb/IIIa), also called TANGO 268. The GPIIb/IIIa polynucleotides
CC and polypeptides and their modulators, e.g. antisense nucleic acids,
CC ribozymes and antibodies, are useful for preventing, treating and
CC diagnosing disorders associated with aberrant expression or activity of
CC GPIIb/IIIa. These disorders include bleeding disorders
CC (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders
CC (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic
CC disorders, coronary artery and cerebral artery diseases (e.g. stroke and
CC ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial
CC infarction), immunological diseases (e.g. platelet disorder) and
CC embryonic liver disorders. Preferably they are used to prevent acute
CC cardiac ischaemia following angioplasty and metastatic cancers,
CC especially of the colon and liver.
XX
XX
SQ Sequence 339 AA;
Query Match 99.7%; Score 1300; DB 22; Length 339;
Best Local Similarity 99.6%; Pred. No. 7; 8e-105;
Matches 248; Conservative 0; Mismatches 1; Indels 3; Gaps 0;

QY 181 VTGTSVTPSPRLPTEPPSSVAEFSEATAEITVSFTNKVFPTTETSRSITTSFKESDSPAGP 240
Db 201 VTGTSVTPSPRLPTEPPSSVAEFSEATAEITVSFTNKVFPTTETSRSITTSFKESDSPAGP 260
QY 241 AROYTTKGN 249
Db 261 AROYTTKGN 269
RESULT 15
ABU11239
13 ABU11239 standard; Protein; 339 AA.
XX
XX AC ABU11239;
XX
DT 06-FEB-2003 (first entry)
XX
DE Glycoprotein VI associated protein sequence #1.
XX
XX Human; mouse; variable heavy; VH; antigen; cancer;
KM complementarity determining region; TANGO 268; glycoprotein VI; GPIIb/IIIa;
KM TANGO 268; extracellular matrix; collagen; platelet release;
KM proliferation; migration; embryogenesis; inflammation; thrombosis;
KM degeneration; thrombocytopenia; antibody; inflammatory disorder;
KM cerebral vascular disease; stroke; ischaemia; venous thromboembolism;
KM leg swelling; pain; ulceration; pulmonary embolism; coronary disease;
KM cardiovascular disease; angina pectoris; myocardial infarction;
KM coronary restenosis; atherosclerosis; immunological disorder;
KM developmental disorder; embryonic disorder; liver disorder;
KM cerebral vascular disease; venous thromboembolism disease.
XX
XX Homo sapiens.
OS
XX WO2002280968-A1.
PN
XX 17-OCT-2002.
PD
XX
XX 09-APR-2002; 2002WO-US11122.
PF
XX
XX 09-APR-2001; 2001US-0929495.
PR
XX
XX (MIL-) MILLENNIUM PHARM INC.
PA
XX Busfield SJ, Villalal C, Jandrot-Perrus M, Vainchencker W, Gill DS;
PI Qian DM, Kingsbury G;
PI
XX WPI; 2003-058477/05.
DR
XX
XX Novel substantially purified antibody immunospecifically binding to
PT TANGO 268 antigen, useful for treating bleeding disorders such as
PT thrombocytopenia, stroke, ischaemia, pulmonary embolism, atherosclerosis
PT
XX
PS Disclosure; Page 222-223; 236pp; English.
XX
XX This invention relates to a novel purified antibody comprising a
CC variable heavy (VH) complementarity determining region (CDR1, VH CDR2
CC or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
CC immunospecifically binding to a TANGO 268 (also referred to as glycoprotein
CC VI (GPIIb/IIIa)) antigen. The antibodies of the invention act to decrease or
CC block TANGO 268 binding to extracellular matrix components, or as a
CC collagen or platelet release and aggregation blocker. The antibodies of
CC the invention are useful for modulating proliferation, migration,
CC morphology, differentiation and/or function of megakaryocytes and
CC platelets, including during development e.g. embryogenesis, modulating
CC leukocyte-platelet and platelet-endothelium interactions in
CC inflammation and/or thrombosis, and modulating platelet aggregation and
CC degranulation. They are also useful for modulating disorders associated
CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
CC migration, morphology, differentiation and/or function, e.g. bleeding
CC disorders such as thrombocytopenia. Other diseases which may be
CC modulated by these antibodies are thrombotic disorders, cerebral
CC vascular diseases (e.g. stroke and ischaemia) venous thromboembolism

CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
 CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
 CC diseases including angina pectoris, myocardial infarction, coronary
 CC stenosis, atherosclerosis, etc); immunological disorders,
 CC developmental disorders, embryonic disorders, liver disorders, cerebral
 CC vascular diseases, venous thromboembolism disease, coronary diseases,
 CC and metastatic cancers. The antibodies of the invention only causes a
 CC transient decrease in platelet counts, platelet aggregation, and/or
 CC platelet activation and so have some advantages over prior art
 CC methods. The present sequence represents a protein sequence used to
 CC create the antibodies of the invention.

XX
 SQ Sequence 339 AA;

Query Match: 99.7%; Score 1300; DB 24; Length 339;
 Best Local Similarity 99.6%; Pred. No. 7.8e-105;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

| | | | |
|----|-----|---|-----|
| QY | 1 | QSGPLPKPSLQALPSSIVPLEKPVTLRCQSPGVJYRLKLSSSRYQDQAVLFIPAKR | 60 |
| | | | |
| Db | 21 | QSGPLPKPSLQVLPSSIVPLEKPVTLRCQSPGVJYRLKLSSSRYQDQAVLFIPAKR | 80 |
| | | | |
| QY | 61 | SLAGRRCSYQNGSLMSLPSDQLEJVAAGVPAKPSLSAQPGPAVSSGGVTLQCCTRYGF | 120 |
| | | | |
| Db | 81 | SLAGRRCSYQNGSLMSLPSDQLEJVAAGVPAKPSLSAQPGPAVSSGGVTLQCCTRYGF | 140 |
| | | | |
| QY | 121 | DQFALYKEGDPAPYKPERWYRASPTITVTAAHSGTYRCYSFSSRDPYLMASPSDPLEL | 180 |
| | | | |
| Db | 141 | DQFALYKEGDPAPYKPERWYRASPTITVTAAHSGTYRCYSFSSRDPYLMASPSDPLEL | 200 |
| | | | |
| QY | 181 | VVTGTSVTPSRLLPTEPPSSVAEFSEATAEELTVSFTNKVFTTETRSITTSFKESDSPAGP | 240 |
| | | | |
| Db | 201 | VVTGTSVTPSRLLPTEPPSSVAEFSEATAEELTVSFTNKVFTTETRSITTSFKESDSPAGP | 260 |
| | | | |
| QY | 241 | ARQYTTKGN | 249 |
| | | | |
| Db | 261 | ARQYTTKGN | 269 |

Search completed: November 10, 2003, 06:16:57
 Job time : 43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 10, 2003, 06:14:09 ; Search time 17 Seconds

(without alignments)
688.803 Million cell updates/sec

Title: US-09-503-387-9

Perfect score: 1304

Sequence: 1 QSGPLPKPSLQALPSSVPL.....SPKESQSPAGPARQYTKGN 249

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 6

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|---------------|--------------------|
| 1 | 333 | 25.5 | 387 | 1 K3S1_HUMAN | Q14943 homo sapien |
| 2 | 322 | 24.7 | 304 | 1 K2S2_HUMAN | P43631 homo sapien |
| 3 | 320.5 | 24.6 | 444 | 1 K3J1_HUMAN | P43629 h killer ce |
| 4 | 315 | 24.2 | 304 | 1 K2S1_HUMAN | Q14954 homo sapien |
| 5 | 314 | 24.1 | 304 | 1 K2S4_HUMAN | P43632 homo sapien |
| 6 | 314 | 24.1 | 348 | 1 K2L1_HUMAN | P43626 h killer ce |
| 7 | 314 | 24.1 | 348 | 1 K2L2_HUMAN | P43627 homo sapien |
| 8 | 312.5 | 24.0 | 341 | 1 K2L3_HUMAN | P43628 h killer ce |
| 9 | 306.5 | 23.5 | 304 | 1 K2S5_HUMAN | Q14953 homo sapien |
| 10 | 302 | 23.2 | 335 | 1 G49B_MOUSE | Q64281 mus musculu |
| 11 | 299 | 22.9 | 287 | 1 FCAR_HUMAN | P24071 homo sapien |
| 12 | 299 | 22.9 | 377 | 1 K2L4_HUMAN | Q99706 homo sapien |
| 13 | 297.5 | 22.8 | 304 | 1 K2S3_HUMAN | Q14952 homo sapien |
| 14 | 294.5 | 22.6 | 455 | 1 K3L2_HUMAN | P43630 homo sapien |
| 15 | 280 | 21.5 | 303 | 1 G49A_MOUSE | Q61450 mus musculu |
| 16 | 143.5 | 11.0 | 495 | 1 A1BG_HUMAN | P04217 homo sapien |
| 17 | 136 | 10.4 | 291 | 1 DN43_DIDMR | P82957 didelphis m |
| 18 | 126.5 | 9.7 | 3707 | 1 PGSM_MOUSE | Q05793 mus musculu |
| 19 | 123.5 | 9.5 | 267 | 1 FCC3_RAT | P27645 rattus norv |
| 20 | 113.5 | 8.7 | 1294 | 1 NRCA_CHICK | P35331 gallus gall |
| 21 | 111.5 | 8.6 | 4391 | 1 PGSM_HUMAN | P98160 homo sapien |
| 22 | 108 | 8.3 | 341 | 1 FCC2_CAVPO | Q60513 cavia porce |
| 23 | 107 | 8.2 | 261 | 1 FCC3_MOUSE | P08508 mus musculu |
| 24 | 106 | 8.1 | 285 | 1 FCC2_RAT | Q61203 rattus norv |
| 25 | 105.5 | 8.1 | 330 | 1 FCC2_MOUSE | P08101 mus musculu |
| 26 | 101 | 7.7 | 1709 | 1 SN_HUMAN | Q9b222 homo sapien |
| 27 | 101 | 7.7 | 3375 | 1 UN52_CAEEL | Q06561 caenorhabdi |
| 28 | 100 | 7.7 | 257 | 1 FCEA_HUMAN | P12319 homo sapien |
| 29 | 100 | 7.7 | 1367 | 1 AMYH_YEAST | P08640 saccharomyc |
| 30 | 99.5 | 7.6 | 727 | 1 PECT1_MOUSE | Q08481 mus musculu |
| 31 | 99 | 7.6 | 739 | 1 VCA1_HUMAN | P19320 homo sapien |
| 32 | 98.5 | 7.6 | 3149 | 1 TEGU_EBV | P03166 epstein-bar |
| 33 | 97.5 | 7.5 | 296 | 1 FCC2_BOVIN | Q28110 bos taurus |

| | | | | | |
|----|------|-----|------|--------------|--------------------|
| 34 | 96.5 | 7.4 | 404 | 1 FCC1_MOUSE | P26151 mus musculu |
| 35 | 96.5 | 7.4 | 1694 | 1 SN_MOUSE | Q62230 mus musculu |
| 36 | 96 | 7.4 | 2774 | 1 MAFA_RAT | P34926 rattus norv |
| 37 | 95.5 | 7.3 | 348 | 1 K1LO_RAT | Q92038 rattus norv |
| 38 | 95.5 | 7.3 | 2282 | 1 ZAN_RABIT | P57999 oryctolagus |
| 39 | 95 | 7.3 | 663 | 1 SEPI_SCHPO | O43058 schizosacch |
| 40 | 95 | 7.3 | 739 | 1 VCA1_MOUSE | P29533 mus musculu |
| 41 | 94.5 | 7.2 | 770 | 1 DAB2_HUMAN | P98082 homo sapien |
| 42 | 94.5 | 7.2 | 912 | 1 ICA5_HUMAN | Q28730 oryctolagus |
| 43 | 94.5 | 7.2 | 1051 | 1 PTK7_CHICK | Q91048 gallus gall |
| 44 | 94.5 | 7.2 | 1443 | 1 NEOL_CHICK | Q90610 gallus gall |
| 45 | 94 | 7.2 | 372 | 1 Y906_MYCTU | Q10562 mycobacteri |

ALIGNMENTS

```
RESULT :
K3S1_HUMAN          STANDARD;          PRT;          387 AA.
ID      K3S1_HUMAN
AC      Q14943;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Killer cell immunoglobulin-like receptor 3DS1 precursor (MHC class I
DE      NK cell receptor) (Natural killer associated transcript 10) (NKAT-10).
CN      KIR3DS1 OR NKAT10.
CS      Homo sapiens (Human).
CC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX      NCBI_TaxID=9606;
RN      1;
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96270004; PubMed=8662091;
RA      Doebring C., Samaridis C., Colonna M.;
RT      "Alternatively spliced forms of human killer inhibitory receptors.";
RL      Immunogenetics 44:227-230(1996).
RN      2;
RP      VARIANT HIS-166.
RX      MEDLINE=98090086; PubMed=9430221;
RA      Liebert M., Valiante N.M., Shum B.P., Shilling H.G.,
RA      Liebert-Weidenbach K., Corliss B., Ryan D., Lanier L.J., Parham P.;
RT      "Human diversity in killer cell inhibitory receptor genes.";
RL      Immunity 7:753-763(1997).
CC      -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC      -!- DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC      -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
EMBL: L76661; AAB36589.1; -.
HSSP: P43626; INKR.
GeneW: HGNC:6340; KIR3DS1.
MIM: 604957; -.
GO: GO:0005887; C: integral to plasma membrane; NAS.
GO: GO:0003793; F: defense/immunity protein activity; NAS.
GO: GO:0030106; F: MHC class I receptor activity; NAS.
GO: GO:0006955; P: immune response; NAS.
GO: GO:0030101; P: natural killer cell activation; NAS.
InterPro: IPR033599; Ig.
InterPro: IPR033006; Ig_MHC.
Pfam: PF00047; Ig_3.
SMART: SM00409; Ig_3.
PROSITE: PS50835; IG_LIKE; FALSE_NEG.
Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
```

KN Repeat; Multigene family; Polymorphism.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 387 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
 FT 3DS1.
 FT DOMAIN 22 346 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 341 360 POTENTIAL.
 FT DOMAIN 361 387 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 42 102 IG-LIKE C2-TYPE 1.
 FT DOMAIN 137 202 IG-LIKE C2-TYPE 2.
 FT DOMAIN 237 300 IG-LIKE C2-TYPE 3.
 FT DISULFID 49 95 BY SIMILARITY.
 FT DISULFID 144 195 BY SIMILARITY.
 FT DISULFID 244 293 BY SIMILARITY.
 FT CARBOHYD 32 92 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 166 166 R -> H.
 FT /FTID=VAR_010377.
 SQ SEQUENCE 387 AA; 42902 MW; 0E75CE730D15E130 CRC64;
 Query Match 25.5%; Score 333; DB 1; Length 387;
 Best Local Similarity 37.3%; Pred. No. 5.2e-19;
 Matches 90; Conservative 26; Mismatches 91; Indels 34; Gaps 7;
 QY 7 KPSLQALPSSLVPLEKPVTRCGGPPGVLYRLEK---LSSRYQDQ-----AVLFI 55
 DB 123 KPSLLAHPPGLVKSGERVILQCSWDIMEHFELHKEMISKDPSRLVGQIHGVSKANFSI 182
 QY 56 PAMKRLSLAGRYRC-----SYQNGSLWSPSDQLELVATGVFAKPSLSAQGPVAVSSGG 108
 DB 183 GSMRRALAGTYRCYGSVTHPPYQ---LSAPSDPLDIIVTGVYEKPSLSAQGPVAVSSGG 238
 QY 109 DVTLOCCQIRYGFDOFALYKEDPAPYKNP-----ERWYRASEPITVTAHSGTYRCYSF 163
 DB 239 SVTLSCSSRSRSDYMYHLRREGAGHERLPAVRKVNRTFQADPFL--GPATHGTYRCYGS 296
 QY 164 SSRDPYJWSAPSDPLELVATGVTSVTPSRLPTEPPSSVAEPSE-----ATAELVTSFTNKV 218
 DB 297 FRHSPYEWSPSDPFLVSVTGNSSSWPSPTEPSSKSGNLRLHLIGTSVVKIPFTILL 356
 QY 219 F 219
 DB 357 F 357
 RESULT 2
 K2S2_HUMAN STANDARD; FRT; 304 AA.
 ID K2S2_HUMAN P43631; Q14955;
 AC P43631; Q14955;
 DT 01-NOV-1995 (Ref. 32, Created)
 DT 16-OCT-2001 (Ref. 40, Last sequence update)
 DT 15-SEP-2003 (Ref. 42, Last annotation update)
 DE Killer cell immunoglobulin-like receptor 2DS2 precursor (K2C class)
 DE NK cell receptor (Natural killer associated transcript 5) (NKAT-5)
 DE (p58 natural killer cell receptor clone C5-49) (p58 NK receptor) (NK
 DE receptor 183 Act1).
 DE KIR2DS2 OR NKAT5.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 OX 1;
 RN RP SEQUENCE OF 2-304 FROM N.A.
 RC TISSUE=Natural killer cells;
 RX MEDLINE=95269128; PubMed=7743980;
 RA Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Mainati M.S.,
 RA Vitale M., Bottino C., Moretta A., Moretta L., Long E.O.;
 RT "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
 RT related molecules with diversity in both the extra- and intracellular
 RT domains."
 RT Immunity 3:439-449(1995).
 RN 12;
 RP SEQUENCE FROM N.A.

RX MEDLINE=95232526; PubMed=7716543;
 RA Colonna M., Samaridis J.;
 RT "Cloning of immunoglobulin-superfamily members associated with HLA-C
 RT and HLA-B recognition by human natural killer cells."
 RT Science 268:405-408(1995).
 RN 13;
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphoid;
 RX MEDLINE=96195217; PubMed=8627176;
 RA Biassoni R., Cantoni C., Falco V., Verdiani S., Bottino C., Vitale M.,
 RA Conte R., Poggi A., Moretta A., Moretta L.;
 RT "The human leukocyte antigen (HLA)-C-specific 'activatory' or
 RT 'inhibitory' natural killer cell receptors display highly homologous
 RT extracellular domains but differ in their transmembrane and
 RT intracytoplasmic portions."
 RT J. Exp. Med. 183:645-650(1996).
 CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
 CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
 CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U24079; AAC50338.1; ALT_INIT.
 CC EMBL; L41347; AAA65225.1; .
 CC EMBL; X89893; CAA61983.1; .
 CC HSSP; P43626; INKR.
 CC Genew; HGNC:6334; KIR2DS2.
 DR MIM; 604953; .
 DR GO; GO:0016021; C:integral to membrane; NAS.
 DR GO; GO:0034888; F:transmembrane receptor activity; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; IG_1.
 DR SMART; SMO0409; IG_1.
 DR PROSITE; PS50835; IG_LIKE; FALSE_NEG.
 KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KW Repeat; Multigene family.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 304 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
 FT 2DS2.
 FT DOMAIN 22 245 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 246 265 POTENTIAL.
 FT DOMAIN 266 304 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 42 107 IG-LIKE C2-TYPE 1.
 FT DOMAIN 142 205 IG-LIKE C2-TYPE 2.
 FT DISULFID 49 100 BY SIMILARITY.
 FT DISULFID 149 198 BY SIMILARITY.
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 20 20 W -> G (IN REF. 3).
 SQ SEQUENCE 304 AA; 33501 MW; 186C77DD9E86BA28 CRC64;
 Query Match 24.7%; Score 322; DB 1; Length 304;
 Best Local Similarity 33.6%; Pred. No. 2.8e-18;
 Matches 93; Conservative 32; Mismatches 94; Indels 58; Gaps 10;
 QY 7 KPSLQALPSSLVPLEKPVTRCGGPPGVLYRLEKLSSSRYQD-----QAVLI 53
 DB 28 KPSLLAHPPGLVKSSEETVILQCSWDVRFHFELHR--EGKYVDTLHLIGEHGVSKANFS 85
 QY 54 FIPAMKRLSLAGRYRC-----SYQNGSLWSPSDQLELVATGVFAKPSLSAQGPVAVSS 106
 DB 86 SIGPMMDLAGTYRCYGSVTHPPYQ---LSAPSDPLDIIVTGVYEKPSLSAQGPVAVLA 141

QY 107 GSDVTLQCTRYGFDQFALYKED-----PAPYKNPERWYRASFPITVTAAHSTYR 159
DB 142 GESVTLSCSSRSSSYDMYHLSREGFAHERFSAQPKVNGT--FQADFFL--GPATHGTYR 197
QY 160 CYSFSSRDPLWASAPSDPLELVGTSTPSRLPTEPPSSVAEFSE-----ATAELTVSF 214
DB 198 CFGSFRDSPYEWSSNSDPLVSVTGNFNSWSPTEPPSSKTGNPRHLHLVLIGTSVVKIPF 257
QY 215 T-----NK---VFTESTRSITSPKESD 235
DB 258 TLLFPLLRMCNKKNAAVMDQEPAGNRRTVNSESD 294

RESULT 3

K3L1_HUMAN STANDARD; PRT; 444 AA.
AC P43629; Q43473; Q16541;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 3D2, precursor (MHC class I
NK cell receptor) (Natural killer killer associated transcript 3) (NKAT-3)
DE (p70 natural killer cell receptor clones C2-2/CL-1) (HLA-BW4 specific
inhibitory NK cell receptor).
GN KIR3DL1 OR NKAT3 OR NK31.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=95232526; PubMed=7716543;
RA Colonna M., Samaridis J.;
RT "Cloning of immunoglobulin-superfamily members associated with HLA-C
and HLA-B recognition by human natural killer cells";
RJ Science 268:405-408(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=9611957; PubMed=8777725;
RA Wagtmann N., Rajagopalan S., Winter C.C., Peruzzi M., Jong E.C.;
RT "Killer cell inhibitory receptors specific for HLA-C and HLA-B
identified by direct binding and by functional transfer";
RJ Immunity 3:801-809(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=96343861; PubMed=8760804;
RA Pende D., Biassoni R., Cantoni C., Verdiani S., Falco M.,
di Donato C., Accame L., Bottino C., Moretta A., Moretta L.;
RT "The natural killer cell receptor specific for HLA-A allotypes: a
novel member of the p58/p70 family of inhibitory receptors that is
characterized by three immunoglobulin-like domains and is expressed
as a 140-kD disulfide-linked dimer";
RJ J. Exp. Med. 184:505-518(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95378652; PubMed=7650366;
RA D'Andrea A., Chang C., Franz-Bacon K., McClanahan T., Phillips J.H.,
Lanier L.L.;
RT "Molecular cloning of NKBL, A natural killer cell receptor for HLA-B
allotypes";
RJ J. Immunol. 155:2306-2310(1995).
RN [5]
RP SEQUENCE FROM N.A. AND VARIANTS.
RX MEDLINE=98090086; PubMed=9430221;
RA Uberg M., Valiante N.M., Stum B.P., Snilling H.G.,
Lienert-Weidenbach K., Corliss B., Ryan D., Lanier L.L., Patham P.;
RT "Human diversity in killer cell inhibitory receptor genes";
RJ Immunity 7:753-763(1997).

CC -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA B4
CC ALLELE. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING
CC CELL LYSIS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL: J41269; AAA69870.1; -
DR EMBL: U30273; AAB52521.1; -
DR EMBL: U30274; AAB52522.1; -
DR EMBL: X94262; CAA63938.1; -
DR EMBL: U31446; AAC23725.1; -
DR EMBL: AF022049; AAB95322.1; -
DR F.R: G01925; G01925.
DR HSSP: P43626; INKR.
DR Genew: HGNC:6338; KIR3DL1.
DR MIM: 604946; -
DR GO: GO:0005887; C:integral to plasma membrane; NAS.
DR GO: GO:0003793; F:defense/immunity protein activity; NAS.
DR GO: GO:0030409; F:HLA-B specific inhibitory MHC class I recep. . .; NAS.
DR GO: GO:0006955; P:immune response; NAS.
DR GO: GO:0030402; P:negative regulation of natural killer cell . . .; NAS.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003006; IG_YMC.
DR Pfam: PF00047; IG_3.
DR SMART: SM00409; IG_3.
DR PROSITE: PSS0835; IG_LIKE; FALSE NEG.
KM Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW Repeat; Multigene family; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 444
FT
FT DOMAIN 22 340
FT TRANSMEM 341 360
FT DOMAIN 361 444
FT DOMAIN 42 102
FT DOMAIN 137 202
FT DOMAIN 237 300
FT DISULFID 49 95
FT DISULFID 144 195
FT DISULFID 244 293
FT CARBOHYD 92 92
FT CARBOHYD 179 179
FT CARBOHYD 273 273
FT VARIANT 2 2
FT VARIANT 13 13
FT VARIANT 23 23
FT VARIANT 68 68
FT VARIANT 75 75
FT VARIANT 259 259
FT VARIANT 333 333
SQ SEQUENCE 444 AA; 49098 MW; 47DEA12BBARDEC53 CRC64;
/FTid=VAR_010319.
L -> F.
/FTid=VAR_010320.
M -> V.
/FTid=VAR_010321.
I -> V.
/FTid=VAR_010322.
I -> L.
/FTid=VAR_010323.
G -> R.
/FTid=VAR_010336.
S -> C.
/FTid=VAR_010324.
/FTid=VAR_010324.
/FTid=VAR_010324.

QY Query Match: 24.6%; Score 320.5; DB 1; Length 444;
Best Local Similarity 38.6%; Pred. No. 5.9e-18;
Matches 83; Conservative 22; Mismatches 81; Indels 29; Gaps 5;
7 KPSLCALPSSLVPLEKPVTLRCGPPGVDLRLLEKLSSSRVQDAV-----LFI 55


```

DB      123 KPSLLAHGGLVKGSGERYILQWSDIMEFHEFLAKEGTSKDPKSLVQGHGVSKANPSI 182
QY      56 PAMKRSIAGRYRC-----SYQNGSLWSLPSCDLEJYATGVFAKPSLSAQGPFAVSS 108
DB      183 GRYMLALAGTYRCYGSVTHPYQ---LSAPSDPLDIVTGPYEKPSLSAQGPFAVSS 238
QY      109 DVTLCQOTRYGFDQFALYKEGDBAPYKNP-----ERWRASFPITVTAAHSGTYRCYSF 163
DB      239 SVTLSCSSRSSYDMYHLSREGGAHERRLPAVRKVNRTFOADPFL--GPATHGTYRCFGS 296
QY      164 SSRDPYLSAPSPDPLVLTGTSVTPSRLLPTEPPS 198
DB      297 FRHSPYEMSDPSDPLVSVTGNPSSSWPSPTEPPSS 331

RESULT 4
K2S1_HUMAN
ID      K2S1_HUMAN          STANDARD;          ERT;          304 AA.
AC      Q14954; Q43471;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Killer cell immunoglobulin-like receptor 2DS1 precursor (MHC class I
DE      NK cell receptor Eb6 Act1).
GN      KIR2DS1.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Lymphoid;
RX      MEDLINE=96195217; Pubmed=8627176;
RA      Biassoni R., Cantoni C., Faico M., Verdiani S., Bottino C., Vitale M.,
RA      Conce R., Poggi A., Moretta A., Moretta L.;
RT      "The human leukocyte antigen (HLA)-C-specific 'activatory' or
RT      'inhibitory' natural killer cell receptors display highly homologous
RT      intracellular domains but differ in their transmembrane and
RT      intracytoplasmic portions.";
RL      J. Exp. Med. 183:645-650(1996).
RN      [2]
RP      SEQUENCE FROM N.A., AND VARIANT LYS-91.
RX      MEDLINE=98090086; Pubmed=9430221;
RA      Uhrberg M., Vainante N.M., Shum B.P., Shilling H.G.,
RA      Lienert-Weidenbach K., Corliss B., Tyan D., Lanier L.L., Pecham P.;
RT      "Human diversity in killer cell inhibitory receptor genes.";
RT      Immunity 7:753-763(1997).
CC      -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC      DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC      -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC      -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation.
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announc/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: X89892; CA61982.1; -.
DR      EMBL: AF022046; AAB95319.1; -.
DR      HSSP: P43626; INKR.
DR      Genew: HGNC:6333; KIR2DS1.
DR      MIM: 604952; -.
DR      GO: GO:0016021; C: integral to membrane; NAS.
DR      GO: GO:0004888; F: transmembrane receptor activity; NAS.
DR      GO: GO:0006955; P: immune response; NAS.
DR      InterPro: IPR003599; IG.
DR      InterPro: IPR003006; IG_MHC.
DR      Pfam: PFC0047; IG_2.

```

```

DR      SMART; SMO0409; IG; 1.
DR      PROSITE; PSS0835; IG_LIKE; FALSE_NEG.
KW      Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW      Repeat; Multigene family; Polymorphism.
FT      SIGNAL      1      21
FT      CHAIN       22      304
FT      DOMAIN      22      245
FT      TRANSMEM    246      264
FT      DOMAIN      265      304
FT      DOMAIN      42      107
FT      DOMAIN      142      205
FT      DISULFID     49      100
FT      DISULFID     149      198
FT      CARBOHYD     67      67
FT      CARBOHYD     84      84
FT      CARBOHYD     144      144
FT      CARBOHYD     178      178
FT      VARIANT     91
FT      SEQUENCE    304 AA; 33646 MW; 4193A542151CAE06 CRC64;
SQ      /FTID=VAR_010318.

Query Match      24.2%; Score 315; DB 1; Length 304;
Best Local Similarity 34.6%; Pred. No. 1e-17;
Matches 84; Conservative 31; Mismatches 90; Indels 38; Gaps 7;

QY      7 KPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLEKLSSRYQD-----QAVL 53
DB      28 KPSLLAHGGLVKGSGERYILQWSDVMEFHEFLHR--EGMFNDTLRLIGHHDGVSKANP 85
QY      54 FIPAMKRSIAGRYRC-----SYQNGSLWSLPSCDLEJYATGVFAKPSLSAQGPFAVSS 106
DB      56 SISRMQDLACTYRCYGSVTHSPYQ---LSAPSDPLDIVTGPYEKPSLSAQGPFAVLA 141
QY      107 GGDVTLQOTRYGFDQFALYKEGDBAPYKNP-----ERWRASFPITVTAAHSGTYRCY 161
DB      142 GENVTLSRSSSSYDMYHLSREGGAHERRLPAVKVNRTFOANPFL--GPATHGTYRCF 199
QY      162 SFSSRDPLYMSAPSPDPLVLTGTSVTPSRLLPTEPPSSVAEFSF-----ATAELTVSFTN 216
DB      200 GSFRDSPYEMSKSDPLVSVTGNPSSNSWSPSPTEPPSSSETGNPRHLVLTGTSVVKLPFTI 259
QY      217 KVF 219
DB      260 LIF 262

RESULT 5
K2S4_HUMAN
ID      K2S4_HUMAN          STANDARD;          ERT;          304 AA.
AC      P43632;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Killer cell immunoglobulin-like receptor 2DS4 precursor (MHC class I
DE      NK cell receptor) (Natural killer cell associated transcript 8) (NKAT-8)
DE      (P58 natural killer cell receptor clone C1-39) (P58 NK receptor) (CL-
DE      17).
GN      KIR2DS4 OR NKAT8 OR KKA3.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Natural killer cells;
RX      MEDLINE=95269128; Pubmed=7749980;
RA      Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Mainati M.S.,
RA      Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT      "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RT      related molecules with diversity in both the extra- and intracellular
RT      domains.";
RL      Immunity 2:439-449(1995).

```



```

RN [2]:
RP SEQUENCE FROM N.A. MEDLINE=96270004; PubMed=8662091;
RX Boehring C., Samaridis J., Colonna M.;
RA "Alternatively spliced forms of human killer inhibitory receptors.";
RL Immunogenetics 44:227-230(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid; MEDLINE=96350503; PubMed=8765026;
RX Bottino C., Sivori S., Vitale M., Cantoni C., Falco M., Perde D.,
RA Morelli L., Augugliaro R., Semenzato G., Biassoni R., Moretta L.,
RA Moretta A.;
RT "A novel surface molecule homologous to the p58/p50 family of
RT receptors is selectively expressed on a subset of human natural
RT killer cells and induces both triggering of cell functions and
RT proliferation.";
RL Eur. J. Immunol. 26:1916-1924(1996).
RN [4]
RP SEQUENCE FROM N.A.
RQ Chan H.W., Salter R.D.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by not-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U24077; AAC50336.1; ALT_INT.
DR EMBL; L76671; AA36599.1; -.
DR EMBL; X94609; CAAB4317.1; -.
DR EMBL; AF022255; AAB61291.1; -.
DR HSSP; P43626; INKR.
DR Genew; HGNC:6336; KIR2DS4.
DR MIM; 604955; -.
DR GO; GO:0005987; C:integral to plasma membrane; TAS.
DR GO; GO:0003822; F:MHC-interacting protein; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_2.
DR SMART; SMC0409; IG_1.
DR PROSITE; PSS0835; IG_LIKE; FALSE_NEG.
KM Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
Repeat; Multigene family.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 304 KILIER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT FT 2DS4.
FT DOMAIN 22 245 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 246 265 POTENTIAL.
FT DOMAIN 266 304 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 422 437 IG-LIKE C2-TYPE 1.
FT DOMAIN 442 455 IG-LIKE C2-TYPE 2.
FT DISULFID 49 100 BY SIMILARITY.
FT DISULFID 149 198 BY SIMILARITY.
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . . ) (POTENTIAL).
SQ SEQUENCE 304 AA; 33583 MW; CEFDFAFF3FD679A3F CRC64;
```

[illegible]

```

RESULT 6
K2L1 HUMAN
ID _K2L1 HUMAN STANDARD; PRT; 348 AA.
AC P43626; O43470;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2DL1 precursor (MHC class I
DE NK cell receptor) (Natural killer associated transcript 1) (NKAT-1)
DE (p58 natural killer cell receptor clones CL-42/47.11) (p58 NK
DE receptor) (p58.1 MHC class-I specific NK receptor).
GN KIR2DL1 OR NKAT1 OR CD158A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=95232526; Pubmed=7716543;
RA Colonna M., Samaridis J.;
RT "Cloning of immunoglobulin-superfamily members associated with HLA-C
RL and HLA-B recognition by human natural killer cells.";
RL Science 268:405-408(1995).
RN [2]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 22-45.
RC TISSUE=Natural killer cells;
RX MEDLINE=95269128; Pubmed=7749980;
RA Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Mainati M.S.,
RA Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RT related molecules with diversity in both the extra- and intracellular
RT domains.";
RT Immunoty 2:439-449(1995).
RN [3]
RP SEQUENCE FROM N.A. AND VARIANTS.
RX MEDLINE=98090086; Pubmed=9430221;
RA Unberg M., Valiante N.M., Shum B.P., Shilling H.G.,
RA Lienert-Weidenbach K., Corliss B., Ryan D., Lanier L.L., Parham P.;
RT "Human diversity in killer cell inhibitory receptor genes.";
RL Immunoty 7:753-763(1997).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 27-221.
RX MEDLINE=97433335; Pubmed=9288975;
RA Fan Q.R., Mosyak L., Winter C.C., Wagtmann N., Long E.O., Wiley D.C.;
RT "Structure of the inhibitory receptor for human natural killer cells
RT resembles haematopoietic receptors.";
RL Nature 389:96-100(1997).
RN [5]
RP FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES
CC INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

```

```

CC -! SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; I41267; AAA69868.1; -
DR EMBL; U24076; AAC50335.1; -
DR EMBL; U24078; AAC50337.1; -
DR EMBL; AF022045; AAB95318.1; -
DR PIR; A56247; A56247.
DR PDB; INKR; 11-NOV-98.
DR PDB; LIM9; 30-MAY-01.
DR Genew; HGNC:6329; KIR2DL1.
DR MIM; 604936; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR003593; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS5035; IG_LIKE; FALSE_NEG.
KM Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KM Repeat; Multigene family; Polymorphism; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 348 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT DOMAIN 22 245 2DL1.
FT TRANSMEM 246 264 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 265 348 POTENTIAL.
FT DOMAIN 42 107 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 142 205 IG-LIKE C2-TYPE 1.
FT DISULFID 49 100 -G-LIKE C2-TYPE 2.
FT DISULFID 149 198
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 5 5 V -> F.
FT VARIANT 37 37 /FTID=VAR_003949.
FT VARIANT 37 37 P -> R.
FT VARIANT 135 135 /FTID=VAR_003950.
FT VARIANT 135 135 P -> L.
FT VARIANT 175 175 /FTID=VAR_003951.
FT VARIANT 175 175 P -> T.
FT VARIANT 184 184 /FTID=VAR_010331.
FT VARIANT 184 184 D -> N.
FT VARIANT 203 203 /FTID=VAR_010332.
FT VARIANT 203 203 H -> R.
FT VARIANT 237 237 /FTID=VAR_010333.
FT VARIANT 237 237 K -> E.
FT VARIANT 266 266 /FTID=VAR_010334.
FT VARIANT 266 266 R -> C.
FT VARIANT 266 266 /FTID=VAR_010335.
FT STRAND 32 34
FT STRAND 38 40
FT TURN 41 42
FT STRAND 45 51
FT STRAND 57 63
FT STRAND 66 73
FT STRAND 75 77
FT TURN 78 79
FT STRAND 80 87
FT HELIX 92 94
FT STRAND 96 104
FT TURN 105 106
FT STRAND 107 107
FT TURN 108 109

```

```

FT STRAND 118 123
FT STRAND 130 134
FT STRAND 138 139
FT TURN 141 142
FT STRAND 144 151
FT STRAND 157 162
FT TURN 163 164
FT STRAND 169 172
FT STRAND 174 177
FT TURN 178 179
FT STRAND 180 189
FT STRAND 194 202
FT TURN 203 204
FT STRAND 205 209
FT STRAND 216 220
SC SEQUENCE 348 AA; 38504 MW; 3DFF2D6FDCED1D E CRC64;

Query Match 24.1%; Score 314; DB 1; Length 348;
Best Local Similarity 32.3%; Pred. No. 1.4e-17;
Matches 93; Conservative 36; Mismatches 105; Indels 54; Gaps 10;

QY 7 KPQLALPSSLVPLEKPVTLRCQPPGVLDYRLKLSRRYQD-----QAVL 53
DB 28 KPQLAHPPPLVKSSEVTILQCSGLDMFEHFLHR--EGMFNDLRLIGEHHDGSKANF 85
QY 54 FIPAMKSLAGRYRC-----SYNGSLMSLPSDQLELVATGVFAKPSLSACPPAVSS 106
DB 86 SISRMTQDLAAGTYRCYGVSTHSPYO---VSAPSPLDIVIGLYEKPSLSAQPPTVLA 141
QY 107 GGDVTLQCOTRYGFDQFALYKEGPAPYKNP-----ERWYRASPIIITVAHSGTYRCY 161
DB 142 GENVTLLSCSSRSYDMYHLSREGSAHERRLPAGPKVNGTFQADPPL--GPATHGTYRCF 199
QY 162 SFSSRDPLYLWSPDPLLVLTGVTTPSRLLPTEPPSSVA-----EFSEATAEIVTSF-- 214
DB 200 GSFDSPYEWKSSDPLLVSVTGPNPSNSWSPSPTEPPSSKTGNPHLHILIGTSVYIIFIL 259
QY 215 -----TNK----VFTTTSRSITTSPKESDSPAGPARQYTKGN 249
DB 260 LFFLLHRWCSNKKAAVMQESAGNRVANSSEDSDE-QDPQEVYTYQLN 306

RESULT 7
K2L2_HUMAN STANDARD; PRT; 348 AA.
ID K2L2_HUMAN Q14951;
AC P43627; Q14951;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2D12 precursor (MHC class I
DE NK cell receptor) (Natural killer associated transcript 6) (NKAT-6)
DE (p58 natural killer cell receptor clone CL-43) (p58 NK receptor).
GN KIR2D12 OR NKAT6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=95269128; PubMed=7749980;
RA Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Mainati M.S.,
RA Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RT related molecules with diversity in both the extra- and intracellular
RT domains.";
RT Immunity 2:439-449(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96270004; PubMed=8662091;
RA Dohring C., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors.";
RL Immunogenetics 44:227-230(1996).

```

```
CC -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C
CC ALLELES. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING
CC CELL LYSIS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U24075; AAC50334.1; -.
DR EMBL: L76669; AAB36597.1; -.
DR PDB: 1EPX; 14-JUN-00.
DR PDB: 2DL2; 29-DEC-99.
DR PDB: 2DL1; 05-MAY-00.
DR Genew; HGNC:6330; KIR2DL2.
DR MIM; 604937; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG_LIKE; FALSE_NEG.
KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW Repeat; Multigene family; 3D-structure.
FT SIGNAL 1 21
FT CHAIN 22 348
FT 22 348 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT 22 348
FT DOMAIN 22 245
FT TRANSMEM 246 264
FT DOMAIN 265 348
FT DOMAIN 42 107
FT DOMAIN 142 205
FT DISULFID 49 100
FT DISULFID 149 198
FT CARBOHYD 84 84
FT CARBOHYD 178 178
FT CARBOHYD 211 211
FT CONFLICT 289 293
SQ SEQUENCE 348 AA; 38472 MW; 5B54C548F5CF3BF CRC64;

Query Match 24.1%; Score 314; DB 1; Length 348;
Best Local Similarity 32.4%; Pred. NO. 1.4e-17;
Matches 94; Conservative 36; Mismatches 102; Indels 58; Gaps 11;

QY 7 KPSIQALPSSIVLEKPVTLRCQGPVDYRLKLSRRYOD-----QAVL 53
DB 28 KPSLAAHPGRJVKSEETVILQWSDVRFHFPLHR--EGKPKDTLHLGHHGVSRAKF 85

QY 54 FIPAMKRSLAGRYRC-----SYQNGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSS 106
DB 86 SIGPMMODLAGTYRCYGSVTHSPYQ---LSAPSDPLDIVITGLYEKPSLSAQPGPTVLA 141

QY 107 GGDVTLQCCRYGFGQFALYKGD-----PAPYKNPERMYRASPIITVTAHSGTYR 159
DB 142 GGSVTLSCSSRSSTDMYHLRSRGEAHECRFSAGPKVNGT--GQADFPL--GPATHGQTYR 197

QY 160 CYSFSSRDPYLSAPSPLLVLTGTSVTPRLPTEPPSSVA-----EFSATAELVQVSF 214
DB 198 CFGSFRDSPYEWSSSDPLLVSVIGNPSNSWSPTEPSSKTGNFRHLHLIGTSTVAVILF 257

QY 215 -----TNK---VFTEFSRSITTSPEKSDSPAGPARQYTKGN 249
DB 258 ILLEFLHRCWCKNAAVVMDQESAGNRTANSEDSDE-QDPQEVITYQLN 306

RESULT 8
K2L3_HUMAN
ID K2L3_HUMAN STANDARD; PRT; 341 AA.
```

```
AC F43628; 043472;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2DL3 precursor (MHC class II
DE NK cell receptor) (Natural killer killer associated transcript 2) (NKAT-2)
DE (p58 natural killer cell receptor clone Cl-6) (p58 NK receptor) (p58.2
DE MHC class-II specific NK receptor).
GN KIR2DL3 OR NKAT2 OR CD158B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
OX 111
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=95269128; PubMed=7749980;
RA Magtman N., Blasson R., Carton C., Verdiani S., Malnati M.S.,
RA Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
RT "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
RT related molecules with diversity in both the extra- and intracellular
RT domains."
RT J Immunol 159:439-449(1995).
RN 131
RP SEQUENCE FROM N.A. AND VARIANTS ALA-9; ARG-32; GLY-56; ARG-71 AND
RP HIS-318.
RX MEDLINE=98090086; PubMed=9430221;
RA Ustberg N., Vallante N.M., Shum B.P., Snijling H.G.,
RA Liebert-Weidenbach K., Corliss B., Tyran D., Lanier L.D., Fatham E.;
RT "Human diversity in killer cell inhibitory receptor genes."
RL Immunity 7:753-763(1997).
CC -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L41268; AAA69869.1; -.
DR EMBL: U24074; AAC50333.1; -.
DR EMBL: AF022048; AAB95321.1; -.
DR PIR; I61725; I61725.
DR HSSP; P43626; INKR.
DR Genew; HGNC:6331; KIR2DL3.
DR MIM; 604938; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_2.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG_LIKE; FALSE_NEG.
KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW Repeat; Multigene family; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 341
FT 22 341 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT 22 341
```

```
FT DOMAIN 22 245 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 246 265 POTENTIAL.
FT DOMAIN 266 341 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 107 IG-LIKE C2-TYPE 1.
FT DOMAIN 142 205 IG-LIKE C2-TYPE 2.
FT DISULFID 45 103 BY SIMILARITY.
FT DISULFID 149 199 BY SIMILARITY.
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 9 9 V -> A.
FT VARIANT 32 32 /FTID=VAR_010313.
FT VARIANT 32 32 U -> R.
FT VARIANT 56 56 /FTID=VAR_010314.
FT VARIANT 56 56 Q -> E.
FT VARIANT 71 71 /FTID=VAR_010315.
FT VARIANT 71 71 H -> R.
FT VARIANT 318 318 /FTID=VAR_010316.
FT VARIANT 318 318 R -> H.
SQ SEQUENCE 341 AA; 37886 MM; C21SAFF80EA9AA32 CRC64;

Query Match 24.0%; Score 312.5; DB 1; Length 341;
Best Local Similarity 37.4%; Pred. No. 1.8e-17;
Matches 82; Conservative 24; Mismatches 76; Indels 37; Gaps 7;

QY 7 KPSLQALPSSLVPLEKPVTLRCQGPVGLYRLEKLSRRYQD-----QAVL 53
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 28 KPSLLAHGPIVXSEETVILQCSVDVRFQHLHR--EGRKDTLHIGEHGVSKANF 85
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 54 FIPAMKRLAGRYRC-----SYNGSLMSLPDQLELVATGVFAKPSLSAQGPVAVSS 106
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 86 SIGPMMDLAGTGRCYGVSHTSYQ---LSAPSDPLDIVITGLYEKPSLSAQGPVTLA 141
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 107 GGEVTLQCTRYGDFQFALYKED-----PAPYKNPERMYRASFPITVTAHSGTYR 159
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 142 GGEVTLSCSSRSYDMYHLSRGEAHERRFSAQPKVNGT--FGACDFPL--GPATHGCTYR 197
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 160 CYSFSSRDPYLMASAPSDPLELVVTGTSVTPSRLPTEPPS 198
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 198 CFSGRDPSPYEMSSDPLVSVTGNPSNSWPSPTPESS 236
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 9
K2S5_HUMAN STANDARD; PRT; 304 AA.
ID K2S5_HUMAN STANDARD; PRT; 304 AA.
AC 014953;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 2D5 precursor (MHC class I
DE NK cell receptor) (Natural killer associated transcript 9) (NKAT9).
GN KIR2D5S OR NKAT9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96270004; PubMed=8662091;
RA Doehring C., Samaridis J., Colonna M.,
RT "Alternatively spliced forms of human killer inhibitory receptors.";
RL Immunogenetics 44:227-230(1996).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLIELES.
CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
```

```
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: L76672; AAB36600.1; -.
DR HSSP: P43626; 1NKR.
DR GeneW: HGNC:6337; KIR2D5S.
DR MIM: 604956; -.
DR GO: GO:0005887; C:integral to plasma membrane; NAS.
DR GO: GO:0030110; F:HLA-C specific inhibitory MHC class I recep. . .; NAS.
DR GO: GO:006955; P:immune response; NAS.
DR InterPro: IPR003599; IG.
DR InterPro: IPR003006; IG_MHC.
DR Pfam: PF00047; IG_2.
DR SMART: SM00409; IG_1.
DR PROSITE: PS50835; IG_LIKE; FALSE NEG.
KM Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KM Repeat; Multigene family.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 304 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT 2D5S.
FT DOMAIN 22 245 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 246 264 POTENTIAL.
FT DOMAIN 265 304 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 107 IG-LIKE C2-TYPE 1.
FT DOMAIN 142 205 IG-LIKE C2-TYPE 2.
FT DISULFID 49 100 BY SIMILARITY.
FT DISULFID 149 198 BY SIMILARITY.
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 304 AA; 33644 MM; FOBD73BFA3DE35DB CRC64;

Query Match 23.5%; Score 306.5; DB 1; Length 304;
Best Local Similarity 36.3%; Pred. No. 4.6e-17;
Matches 78; Conservative 26; Mismatches 82; Indels 29; Gaps 5;

QY 7 KPSLQALPSSLVPLEKPVTLRCQGPVGLYRLEKLSRRYQDQAV-----LFI 55
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 28 KPSLLAHGPIVXSEETVILQCSVDVMEFHLHREGTFNHTLHIGEHIDGVSKNFSI 87
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 56 PAMKRLAGRYRC-----SYNGSLMSLPDQLELVATGVFAKPSLSAQGPVAVSSGG 108
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 86 GRMTQDLAGTGRCYGVSHTSPYQ---LSAPSDPLDIVITGLYEKPSLSAQGPVTLAGE 143
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 109 DVTLQCTRYGDFQFALYKEDDPAPYKNP-----EAYRASFPITVTAHSGTYRCYSF 163
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 144 SVTLSCSSRSYDMYHLSRGEAHERRLPAGPKVNTFGACSDPLPAT--HGAYRCFGS 201
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

QY 164 SSRDPYLMASAPSDPLELVVTGTSVTPSRLPTEPPS 198
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
DB 202 FRDSPYEMSSKSDPLVSVTGNSSNSWPSPTPESS 236
    |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||

RESULT 10
G49B_MOUSE STANDARD; PRT; 335 AA.
ID G49B_MOUSE STANDARD; PRT; 335 AA.
AC 064281; 064312;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Mast cell surface glycoprotein G49B precursor.
GN G49B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS GP49B1 AND GP49B2).
RC STRAIN=C3H, and BALB/c; TISSUE=Bone marrow;
RX MEDLINE=94179223; PubMed=8132564;
RA Castells M.C., Wu X., Arm J.P., Austen K.F., Katz H.R.;
```

```

RT "Cloning of the gp49B gene of the immunoglobulin superfamily and
RT demonstration that one of its two products is an early-expressed mast
RT cell surface protein originally described as gp49."
RL J. Biol. Chem. 269:8393-8401(1994).
CC -!- FUNCTION: MAY PLAY A ROLE IN CELL-CELL OR CELL-CYTOKINE
CC INTERACTIONS DURING THE DEVELOPMENT OF MAST CELLS FROM MULTIPOTENT
CC PROGENITORS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=GP49B1;
CC IsoId=Q64281-1; Sequence=Displayed;
CC Name=GP49B2;
CC IsoId=Q64281-2; Sequence=VSP 002510, VSP 002511;
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U05266; AAA17759.1; -
DR EMBL; U05265; AAA17797.1; -
DR EMBL; U05265; AAA17798.1; -
DR EMBL; U05264; AAA17796.1; -
DR FIR; A53434; A53434.
DR FIR; B53434; B53434.
DR HSSP; P43626; INKR.
DR MGD; MGI:102701; GP49b.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR03006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR PROSITE; PS00835; IG_LIKE; 1.
DR Signal; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KM Alternative splicing.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 335 MAST CELL SURFACE GLYCOPROTEIN GP49B.
FT DOMAIN 24 238 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 239 260 POTENTIAL.
FT DOMAIN 261 335 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 125 IG-LIKE C2-TYPE 1.
FT DOMAIN 124 212 IG-LIKE C2-TYPE 2.
FT DISULFID 49 98 POTENTIAL.
FT DISULFID 144 196 POTENTIAL.
FT CARBOHYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 232 232 G -> D (in isoform GP49B2).
FT VARSPLIC 233 232 /FTid=VSP_002510.
FT VARSPLIC 233 271 Missing (in isoform GP49B2).
FT VARSPLIC 233 271 /FTid=VSP_002511.
SQ SEQUENCE 335 AA; 37544 MW; 6005186D524E7876 CRC64;
Query Match 23.2%; Score 302; DB 1; Length 335;
Best Local Similarity 33.3%; Pred. No. 1.2e-16;
Matches 77; Conservative 36; Mismatches 96; Indels 22; Gaps 5;
QY 1 QSGPLPKPSIQALPSSLVPLEKPVTLRCQGPVGLYRLKLUSSRRYD-----QA 51
DB 22 QAGHLPRPIIAEPGSAIAATSVITWCQSGSAQYHLYKEKSVNFWDPVPLETRKA 81
QY 52 VLFIPAMKRSIAGRYRCSYQNSLSMLSPDCLVATGVFAKPSLSAQPGRAVSSGGDVT 111
DB 82 KENIPSMITSGYGIKYCYESAAGFSEHSDAMELVNIGAVENPSLSVPSNVTSGVSI 141
QY 112 LQCGTRRGFDQFALYKEG-----DPAPYKNPERWYRASEPIITVTAHSGTYRCYSF 163
DB 142 FSCSSSIVFGRFILIQGKGHLSWTLDSQHQNQPSY--ATFVLDAVTPEHNGTFRCYGY 199
QY 164 SSRDPYLMASPSDPLVLTGTSTVTPSRLLPEPSSVAEFSEACTAEJVSF 214

```

```

DB 200 FRNEPQWMSKPSNLSLDMISRTK-DQSSPTPE--DGLFTYQXILIGLVVSF 247
RESULT 11
FCAR_HUMAN STANDARD; PRT; 287 AA.
AC P24071; Q13603; Q13604; Q15727; Q15728; Q92590;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Immunoglobulin alpha Fc receptor precursor (Iga Fc receptor) (CD89
DE antigen).
GN FCAR OR CD89.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A.1).
RX MEDLINE=91079769; PubMed=2258698;
RA Maliszewski C.R., March C.C., Schoenborn M.A., Gimpel S., Shen L.;
RT "Expression cloning of a human Fc receptor for Iga.";
RL J. Exp. Med. 172:1665-1672(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM A.1).
RC TISSUE=Bone marrow;
RX MEDLINE=95363085; PubMed=7636188;
RA de Wit T.P.M., Morton H.C., Capel P.J.A., van de Winkel J.G.C.;
RT "Structure of the gene for the human myeloid Iga Fc receptor (CD89).";
RL J. Immunol. 155:1203-1209(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS A.2 AND A.3).
RC TISSUE=Alveolar macrophage, and Monocytes;
RX MEDLINE=96247667; PubMed=8666819;
RA Parry C., Sibille Y., Lehen A., Monteiro R.C.;
RT "Identification of Fc alpha receptor (CD89) isoforms generated by
RT alternative splicing that are differentially expressed between blood
RT monocytes and alveolar macrophages.";
RL J. Immunol. 156:4442-4448(1996).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS B AND B-DELTA-S2).
RA van Dijk T.B., Morton H.C., Caldenhoven E., Bracke M.,
RA Raaijmakers J.A.M., Lamers J.W.J., Koenderman L., Groot R.P.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM A.3).
RX MEDLINE=96433090; PubMed=8836118;
RA Plass R.J., Andrews P.D., Kerr M.A., Woolf J.M.;
RT "Alternative splicing of the human Iga Fc receptor CD89 in
RT neutrophils and eosinophils.";
RL Biochem. J. 318:771-777(1996).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM UC2).
RA Toyabe S., Kuwano Y., Takeda K., Uchiyama M., Abo T.;
RT "Alternatively spliced forms of monocyte Iga Fc receptors in patients
RT with Iga nephropathy.";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SUBUNITS.
RX MEDLINE=94375887; PubMed=7522255;
RA Pfeifferkorn L.C., Yeaman G.R.;
RT "Association of Iga-Fc receptors (Fc alpha R) with Fc epsilon RI
RT gamma 2 subunits in U937 cells. Aggregation induces the tyrosine
RT phosphorylation of gamma 2.";
RL J. Immunol. 153:3228-3236(1994).
CC -!- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULINS ALPHA.
CC MEDIATES SEVERAL FUNCTIONS INCLUDING CYTOKINE PRODUCTION.
CC -!- SUBUNIT: ASSOCIATES WITH THE FC EPSILON RI GAMMA 2 RECEPTOR
CC INDUCING TYROSINE PHOSPHORYLATION OF GAMMA 2.
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (FORM A) AND SOLUBLE
CC (FORM B).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;

```

```
CC Comment=Additional isoforms seem to exist;
CC Name=A.1;
CC IsoId=P24071-1; Sequence=Displayed;
CC Name=A.2;
CC IsoId=P24071-2; Sequence=VSP_002635;
CC Name=A.3; Synonyms=RIA2;
CC IsoId=P24071-3; Sequence=VSP_002634;
CC Name=B;
CC IsoId=P24071-4; Sequence=VSP_002636;
CC Name=B-delta-S2;
CC IsoId=P24071-5; Sequence=VSP_002632, VSP_002636;
CC Name=U02;
CC IsoId=P24071-6; Sequence=VSP_002633, VSP_002635;
CC TISSUE SPECIFICITY: DIFFERENTIALLY EXPRESSED BETWEEN BLOOD AND
CC MUCOSAL MYELOID CELLS. MONOCYTES EXPRESS ISOFORMS A.1, A.2 AND A.3
CC WHILE ALVEOLAR MACROPHAGES EXPRESS A.1 AND A.2 TRANSCRIPTS;
CC HOWEVER THEY EXPRESS ONLY ONE ISOFORM AT THEIR SURFACES.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -1- DATABASE: NAME=PROW; NOTE=CD guide C083 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/c083.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X54150; CAA38089.1; -.
DR EMBL; X87767; CAA61039.1; -.
DR EMBL; X87768; CAA61039.1; JOINED.
DR EMBL; X87769; CAA61039.1; JOINED.
DR EMBL; X87766; CAA61039.1; JOINED.
DR EMBL; X87765; CAA61039.1; COINED.
DR EMBL; U43774; AAC50639.1; -.
DR EMBL; U43677; AAC50595.1; -.
DR EMBL; U56236; AAB00566.1; -.
DR EMBL; U56237; AAB00567.1; -.
DR EMBL; S82919; AAB14421.1; -.
DR EMBL; D87859; BAA13477.1; -.
DR PIR; G02630; G02630.
DR PIR; JH0332; JH0332.
DR HSSP; P43626; INKR.
DR Genew; HGNC:3608; FCAR.
DR MIM; 147045; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG_2.
DR PROSITE; PS50835; IG_LIKE; FALSE NEG.
KW Receptor; Glycoprotein; Transmembrane; IGA-binding protein;
KW Immunoglobulin domain; Repeat; Signal; Alternative splicing.
FT SIGNAL 1 21
FT CHAIN 22 287
FT DOMAIN 22 227
FT TRANSMEM 228 246
FT DOMAIN 247 287
FT DOMAIN 42 107
FT DOMAIN 139 200
FT DISULFID 49 100
FT DISULFID 146 193
FT CARBOHYD 65 65
FT CARBOHYD 79 79
FT CARBOHYD 141 141
FT CARBOHYD 177 177
FT CARBOHYD 186 186
FT CARBOHYD 196 196
FT VARSPLIC 12 23
FT -----
/FTId=VSP_002632.
```

```
FT VARSPLIC 24 24 G -> GRYISEHFWCRSLGCPNVNDASAQRPG (in
FT isoform U02).
FT /FTId=VSP_002633.
FT VARSPLIC 121 216 Missing (in isoform A.3).
FT /FTId=VSP_002634.
FT VARSPLIC 195 216 Missing (in isoform A.2 and isoform U02).
FT /FTId=VSP_002635.
FT VARSPLIC 217 287 DSIHQDYTTQNLIRMAVAGLVVAJLAITLVEMHSHALNK
FT EASADVAEBSWSQMCQGLTFARTPSVCK -> GRYRPVQ
FT PCVWVGCPGPCHRAGI (in isoform B and
FT isoform B-delta-S2).
FT /FTId=VSP_002636.
SQ SEQUENCE 267 AA; 32265 MW; A2CCA68467CD45F7 CRC64;
Query Match 22.9%; Score 299; DB 1; Length 287;
Best Local Similarity 36.4%; Pred. No. 1.7e-15;
Matches 71; Conservative 34; Mismatches 78; Indels 12; Gaps 2;
QY 1 QSGFLPKPSLQALPSSLVPLEKPYTLRCQGPVGLYRLKLSRRYOD----- 49
DQ 22 QEGDFPMPFISAKSSPVIPLDGSKVIQCCQAIAREAVLTQLMILNSTRYREIGRRLKFWNET 51
QY 50 QAVLFIPAMKRSLAGRYRCSCYNLSLPSDQLELVATGVFAKPSLSAQPGPAVSSGSD 109
DQ 82 DPEFVIDHMDANKAGRYQCQYRHYFRYSDDLVLVTGLYKRPFLSADRGVLMPGEN 141
QY 110 VTLCQTRY-GFDQFALYKEDGAPAYKNPERWYRASFPITVTAAHSGTYRCYSPSSRDP 166
DQ 142 ISLTGSSAHIPFDRPSLAKEGELSLPQHSGSEHPANFSIGPVNLVNSGIYRCYGVWYNRSP 201
QY 169 YLMSAPSDPLELVVT 183
DQ 202 YLMSFPSPNALELVVT 216
RESULT 12
K2L4_HUMAN STANDARD; PRT; 377 AA.
ID K2L4_HUMAN
AC Q99706; O14621; O14622; O14623; O14624; O43534; P78400; P78401;
AC Q99559; Q99560; Q99561; Q99562; Q9UQJ7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor K2L4 precursor (MHC class I
DE NK cell receptor KIR103AS) (Killer cell inhibitory receptor 103AS)
DE (KIR-103AS) (G9P).
GN KIR2DL4 OR KIR103AS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97102173; PubMed=8946682;
RA Selvakumar A., Steffens U., Dupont B.;
RT "NK cell receptor gene of the KIR family with two Ig domains but
RT highest homology to KIR receptors with three Ig domains.";
RL Tissue Antigens 48:285-294 (1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4 AND 5).
RX MEDLINE=97378880; PubMed=9234477;
RA Selvakumar A., Steffens U., Palanisamy N., Chaganti R.S.K., Dupont B.;
RT "Genomic organization and allelic polymorphism of the human killer
RT cell inhibitory receptor gene KIR103.";
RL Tissue Antigens 49:564-573 (1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 6).
RC TISSUE=Lymphoid;
RA Blassoni R.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. AND VARIANTS.
RX MEDLINE=98090086; PubMed=9430221;
```



```

RA Uhrberg M., Valiante N.M., Stum E.P., Shilling H.G.,
RA Lienert-Weidenbach K., Corliss B., Ryan D., Lanier L.L., Parham P.;
RA "Human diversity in killer cell inhibitory receptor genes.";
RA Immunity 7:753-763(1997).
RN [5]
RP SEQUENCE FROM N.A.
RA Chan H.W., Salter R.D.;
RT "Exon deletion contributes to structural diversity of 2D4 killer
RT inhibitory receptors.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=97213129; Pubmed=9059894;
RA Selvakumar A.;
RT "Polymorphism and domain variability of human killer cell inhibitory
RT receptors.";
RL Immunol. Rev. 155:183-196(1997).
CC -|- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=1;
CC IsoId=Q99706-1; Sequence=Displayed;
CC Name=2; Synonyms=AST;
CC IsoId=Q99706-2; Sequence=VSP_002609;
CC Name=3; Synonyms=AS;
CC IsoId=Q99706-3; Sequence=VSP_002610;
CC Name=4; Synonyms=ASD1;
CC IsoId=Q99706-4; Sequence=VSP_002609, VSP_002610;
CC Name=5; Synonyms=ASD2;
CC IsoId=Q99706-5; Sequence=VSP_002609, VSP_002610, VSP_002611;
CC Name=6;
CC IsoId=Q99706-6; Sequence=VSP_002608, VSP_002609, VSP_002610;
CC -|- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -|- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC
DR EMBL; U71199; AAB49756.1; -
DR EMBL; AF003123; AAB61926.1; -
DR EMBL; AF003116; AAB61926.1; JOINED.
DR EMBL; AF003117; AAB61926.1; JOINED.
DR EMBL; AF003118; AAB61926.1; JOINED.
DR EMBL; AF003119; AAB61926.1; JOINED.
DR EMBL; AF003121; AAB61926.1; JOINED.
DR EMBL; AF003122; AAB61926.1; JOINED.
DR EMBL; AF003120; AAB61926.1; JOINED.
DR EMBL; AF002979; AAB71387.1; -
DR EMBL; AF002980; AAB71388.1; -
DR EMBL; AF002981; AAB71389.1; -
DR EMBL; AF002982; AAB71390.1; -
DR EMBL; X97229; CAA65868.1; -
DR EMBL; X99479; CAA67842.1; -
DR EMBL; X99480; CAA67843.1; -
DR EMBL; X99481; CAA67844.1; -
DR EMBL; AF034771; AAB95164.1; -
DR EMBL; AF034772; AAB95165.1; -
DR EMBL; AF034773; AAB95166.1; -
DR EMBL; AF110035; AAD24763.1; -
DR EMBL; AF110032; AAD24763.1; JOINED.
DR EMBL; AF110033; AAD24763.1; JOINED.
DR EMBL; AF110034; AAD24763.1; JOINED.
DR EMBL; U73394; AAC51146.1; -
DR Genew; HGNC:6332; KIR2DL4.
DR MIM; 604945; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.

```

| DR | GO:0004888; F:transmembrane receptor activity; TAS. |
|----|--|
| DR | GO:0006968; P:cellular defense response; TAS. |
| DR | GO:0007165; P:signal transduction; TAS. |
| DR | InterPro: IPR003006; Ig_MHC. |
| DR | Pfam: PF00047; Ig_2. |
| DR | PROSITE; PS50835; IG_LIKE; FALSE_NEG. |
| KW | Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane; |
| KW | Repeat; Multigene family; Alternative splicing; Polymorphism. |
| FT | SIGNAL 1 21 BY SIMILARITY. |
| FT | CHAIN 22 377 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR 2DL4. |
| FT | DOMAIN 22 242 EXTRACELLULAR (POTENTIAL). |
| FT | TRANSMEM 243 263 POTENTIAL. |
| FT | DOMAIN 264 377 CYTOPLASMIC (POTENTIAL). |
| FT | DOMAIN 44 204 IG-LIKE C2-TYPE 1. |
| FT | DOMAIN 139 202 IG-LIKE C2-TYPE 2. |
| FT | DISULFID 51 97 BY SIMILARITY. |
| FT | DISULFID 146 195 BY SIMILARITY. |
| FT | CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL). |
| FT | VARSPLIC 27 121 Missing (in isoform 6). |
| FT | VARSPLIC 219 235 /FTid=VSP_002608. |
| FT | VARSPLIC 219 235 Missing (in isoform 2, isoform 4, isoform 5 and isoform 6). |
| FT | VARSPLIC 236 270 /FTid=VSP_002609. |
| FT | VARSPLIC 271 286 Missing (in isoform 3, isoform 4, isoform 5 and isoform 6). |
| FT | VARSPLIC 271 286 /FTid=VSP_002610. |
| FT | VARSPLIC 271 286 Missing (in isoform 5). |
| FT | VARSPLIC 271 286 /FTid=VSP_002611. |
| FT | VARSPLIC 271 286 Y -> C. |
| FT | VARSPLIC 271 286 /FTid=VAR_010307. |
| FT | VARSPLIC 271 286 Z -> V. |
| FT | VARSPLIC 271 286 /FTid=VAR_010308. |
| FT | VARSPLIC 271 286 T -> A. |
| FT | VARSPLIC 271 286 /FTid=VAR_010309. |
| FT | VARSPLIC 271 286 A -> P. |
| FT | VARSPLIC 271 286 /FTid=VAR_010310. |
| FT | VARSPLIC 271 286 D -> N. |
| FT | VARSPLIC 271 286 /FTid=VAR_010311. |
| FT | VARSPLIC 271 286 H -> N. |
| FT | VARSPLIC 271 286 /FTid=VAR_010312. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010313. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010314. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010315. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010316. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010317. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010318. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010319. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010320. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010321. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010322. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010323. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010324. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010325. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010326. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010327. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010328. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010329. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010330. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010331. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010332. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010333. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010334. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010335. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010336. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010337. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010338. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010339. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010340. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010341. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010342. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010343. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010344. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010345. |
| FT | VARSPLIC 271 286 T -> P (IN REF. 5). |
| FT | VARSPLIC 271 286 /FTid=VAR_010346. |
| FT | VARS |


```

DE Killer cell immunoglobulin-like receptor 2D3 precursor (MHC class I
DE NK cell receptor) (Natural killer associated transcript 7) (NKAT-7).
GN KIR2DS3 OR NKAT7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96270004; PubMed=8662091;
RA Doehring C., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors.";
RL Immunogenetics 44:227-230(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RA Biassoni R.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC -1- SUBCELLULAR LOCATION: TYPE 1 membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb.ch).
CC -----
DR EMBL, L76670; AAB36598.1; -.
DR EXBL, X97231; CAA65870.1; -.
DR HSSP, P43626; INKR.
DR Genew; HGNC:6335; KIR2DS3.
DR MIM: 604954; -.
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0003822; F: MHC-interacting protein; TAS.
DR GO; GO:000668; P: cellular defense response; TAS.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_2.
DR SMART; SMC0409; Ig_1.
DR PROSITE; PS50835; IG_LIKE; FALSE_NEG.
KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW Repeat; Multigene family.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 304 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
FT 2D3.
FT DOMAIN 22 245 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 246 264 POTENTIAL.
FT DOMAIN 265 304 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 42 107 IG-LIKE C2-TYPE 1.
FT DOMAIN 142 205 IG-LIKE C2-TYPE 2.
FT DISULFID 49 103 BY SIMILARITY.
FT DISULFID 149 198 BY SIMILARITY.
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 304 AA; 33717 MW; 80693F79844F9E7E CRC64;

Query Match: 22.8%; Score 297.5; DB 1; Length 304;
Best Local Similarity 36.5%; Pred. No. 2.3e-16;
Matches 83; Conservative 24; Mismatches 78; Indels 37; Gaps 7;

```

```

QY 7 KPSLQALPSSVPLEKPYTLRCQGFPGVDLYRLEKSSSRVQD-----QAVL 53
DB 28 KPSLAHGRGLVKSSEIVYLQWSDVYVHEHFLHR--EGTNDTLRLIGEHIDGVSKANF 85
QY 54 FIPAMKRSLSAGRRC-----SYONSLSLSJSSDQLELVATGVFAKESLSAOPGPAVSS 106
DB 86 SIGMRQDLAAGTYRCYGVPHSPYC-----FSAPSDPLDIVITGTLYEKPSLSAQGPVLA 141

RESULT 14
K3L2_HUMAN STANDARD; PR7; 455 AA.
AC P43630; Q13238; Q14947; Q14948; Q92684; Q95367;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 3DL2 precursor (MHC class I
DE NK cell receptor) (Natural killer associated transcript 4) (NKAT-4)
DE (p70 natural killer cell receptor clone CL-5).
GN KIR3DL2 OR NKAT4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=95232526; PubMed=7716543;
RA Colonna M., Samaridis J.;
RT "Cloning of immunoglobulin-superfamily members associated with HLA-C
RT and HLA-B recognition by human natural killer cells.";
RL Science 268:405-408(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=96111967; PubMed=8777725;
RA Wagtmann N., Rajagopalan S., Wirtz C.C., Peruzzi M., Long E.C.;
RT "Killer cell inhibitory receptors specific for HLA-C and HLA-B
RT identified by direct binding and by functional transfer.";
RL Immunity 3:801-809(1995).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT VAL-113.
RC TISSUE=Lymphoid;
RX MEDLINE=96343861; PubMed=8760804;
RA Pende D., Biassoni R., Cantoni C., Verdiani S., Falco M.,
RA di Donato C., Accame L., Bottino C., Moretta A., Moretta L.;
RT "The natural killer cell receptor specific for HLA-A allotypes: a
RT novel member of the p58/p70 family of inhibitory receptors that is
RT characterized by three immunoglobulin-like domains and is expressed as
RT a 140-kD disulphide-linked dimer.";
RL J. Exp. Med. 184:505-518(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=96270004; PubMed=8662091;
RA Doehring C., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors.";
RL Immunogenetics 44:227-230(1996).
RN [5]
RP VARIANTS ALA-40; VAL-113; ASP-158; HIS-166; PRO-223 AND THR-252.
RX MEDLINE=98090086; PubMed=9430221;
RA Uhrberg M., Valiante N.M., Shum B.P., Shilling H.G.,
RA Hienert-Weidenbach K., Corliss B., Ryan D., Lantier J., Parham P.;
RT "Human diversity in killer cell inhibitory receptor genes.";
RL Immunity 7:753-763(1997).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-A ALLELES.
CC INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC -1- SUBCELLULAR LOCATION: TYPE 1 membrane protein.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

```

CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; L41270; AAA69871.1; -
DR EMBL; U30272; AAB52520.1; -
DR EMBL; X93595; CAA63791.1; -
DR EMBL; X94373; CAA64150.1; -
DR EMBL; L76665; AAB36593.1; -
DR EMBL; L76666; AAB36594.1; -
DR HSSP; P43626; INKR.
DR Genew; HGNC:6339; KIR3DL2.
DR MIM; 604947; -
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0003822; F: MHC-interacting protein; TAS.
DR GO; GO:0006968; P: cellular defense response; TAS.
DR InterPro; IPR003599; I9.
DR InterPro; IPR003006; I9_MHC.
DR Pfam; PF00047; I9; 3.
DR SMART; SM00409; I9; 2.
DR PROSITE; PS50835; IG_LIKE; FALSE_NEG.
KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
KW Repeat; Multigene family; Polymorphism.
FT SIGNAL 1 21
FT CHAIN 22 455
FT FT 22 455
FT FT 22 455
FT DOMAIN 22 340
FT TRANSMEM 341 360
FT DOMAIN 361 455
FT DOMAIN 42 102
FT DOMAIN 137 202
FT DOMAIN 237 300
FT DISULFID 49 95
FT DISULFID 144 195
FT DISULFID 244 293
FT CARBOHYD 179 179
FT CARBOHYD 239 239
FT CARBOHYD 273 273
FT CARBOHYD 306 306
FT VARIANT 40 40
FT FT 113 113
FT FT 158 158
FT VARIANT 166 166
FT VARIANT 228 228
FT VARIANT 252 252
SQ SEQUENCE 455 AA; 50230 MW; DB3A6BBB3C2945 CRC64;

Query Match 22.6%; Score 294.5; DB 1; Length 455;
Best Local Similarity 32.6%; Pred. No. 6.6e-16;
Matches 89; Conservative 35; Mismatches 104; Indels 45; Gaps 10;

QY 3 GPLPKPSLQALPSSIVPLEKPYTLRCQPPGVLYRLKLSSSR-----YQDQAVL- 53
DB 24 GGQDKPFLSARSTVPRGSHVALQCHYRRGNFMFLYKEDRSHVPIFHGRIFQESFIMG 83
QY 54 -FIPAMKRSLAGRYRCSYQNGS-----WSLPDQLELVATGVFAKPSLSAQGPAAVSS 106
DB 84 PVTPAH---AGTYRC---RGRPHSLTGWGAPSNPLVIMVTGNHRKPSLLAHFGLPLKS 136
QY 107 GSDVTLQCCQTRVGFQDFALYKGGDPAPYKXPERMY-----RASPIITVTAHSGTY 158
DB 137 GETVILQCGSDVMFEHFFLHRGIS---EDPSRLVGQIHGYSKANFS:GPLMPVLACTY 193
QY 159 RCYSFSSRDPEYLSAPSDPLELVVTGTSTVPSRLPTPEPSSVAEFSEATAEULTVSTNKV 218

DB 194 RCYGSVPHSPYQLSAPSDPDLVITGLYEKPS-LSAQGPPTVQAGENVTLSCSSWSSYD: 252
QY 219 FTTET-----SRSTITSPK-----ESDGPAGPA 241
DB 253 YHLSRGEAHERRLRAVPKYNRTFQADFFLGP 285

RESULT 15
G49A_MOUSE STANDARD; PRT; 303 AA.
ID G49A_MOUSE
AC 061450;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, last sequence update)
DT 15-SEP-2003 (Rel. 42, last annotation update)
DE Mast cell surface glycoprotein GP49A precursor.
GN GP49A OR GP49.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 24-45.
RC STRAIN=BALB/C; TISSUE=Bone marrow;
RX MEDLINE=91340742; PubMed=1714901;
RA Arm J.P., Gurish M.F., Reynolds D.S., Scott H.C., Gartner C.S.,
RA Austen K.F., Katz H.R.;
RT "Molecular cloning of gp49, a cell-surface antigen that is
RT preferentially expressed by mouse mast cell progenitors and is a new
RT member of the immunoglobulin superfamily.";
RL J. Biol. Chem. 266:15966-15973(1991).
CC -1- FUNCTION: MAY PLAY A ROLE IN CELL-CELL OR CELL-CYTOKINE
CC INTERACTIONS DURING THE DEVELOPMENT OF MAST CELLS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

DR EMBL; M65027; AAA37479.1; -
DR PIR; A40807; A40807.
DR HSSP; P43626; INKR.
DR MGD; MGI:102702; Gp49a.
DR InterPro; IPR007110; IG_Like.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Signal; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 303
FT DOMAIN 24 238
FT TRANSMEM 239 260
FT DOMAIN 261 303
FT DOMAIN 42 125
FT DOMAIN 124 212
FT DISULFID 49 98
FT DISULFID 144 196
FT CARBOHYD 79 79
FT CARBOHYD 133 133
FT CARBOHYD 191 191
SQ SEQUENCE 303 AA; 34194 MW; D165659BFA9C40D CRC64;

Query Match 22.5%; Score 280; DB 1; Length 303;
Best Local Similarity 32.1%; Pred. No. 5.5e-15;
Matches 75; Conservative 35; Mismatches 96; Indels 28; Gaps 5;

QY 1 QSGPLPKPSLQALPSSIVPLEKPYTLRCQPPGVLYRLKLSSSRYQDQAV----- 52
DB 22 QAGHLPKPIIWAEPGSVIAAYTSYIICWGSWEAQYYLLDKESVNPWCTEVLERNKT 81
QY 53 -LFIAMKRSLAGRYRCSYQNGSLSPDQLELVATGVFAKPSLSAQGPAAVSSGSDVT 111

Db 82 KFKIRFMTASYAGIYNKYKSAAGFSEHSDAMELVMTGAYENPSSLVFPSSNVTSSVSIS 141
QY 112 JOCOTRYGFDDPZALYKEGDPAPYKNPERW-----YRASFPITVTAAHSGTYRC 160
Db 142 FKCSSSTLFGRFILIOEG-----KHGLSWTLDSCQANOPTHTATFVLDVAVAPNHNSTFRG 196
QY 161 YSFSSRDPIYJMSAPSPLELVVGTSTVTPSRLPTEPPSSVAEPESEATAELTVSF 214
Db 197 YSFFRNEPQVWSKPSNSLDLMISSTK-EQSCPTPE--DGJFTYQKILIGLVVSF 247

Search completed: November 10, 2003, 06:16:04
Job time : 19 secs

Best Local Similarity 100.0%; Pred. No. 2.3e-111;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 QSGPLPKPSLQALPSSSLVPLEKPVTLRCQSPGVLDLYRLEKLSSSSRYPQDAVLFIIPAMKR 60
    |||
Db 21 QSGPLPKPSLQALPSSSLVPLEKPVTLRCQSPGVLDLYRLEKLSSSSRYPQDAVLFIIPAMKR 80
QY 61 SLAGRYRCGYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCCQTRYGF 120
    |||
Db 81 SLAGRYRCGYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCCQTRYGF 140
QY 121 DQFALYKEGDPAPYKMPERWYRASFPITVTAHSGTYRCYSSSRDPYLWSAPSDPLEL 180
    |||
Db 141 DQFALYKEGDPAPYKMPERWYRASFPITVTAHSGTYRCYSSSRDPYLWSAPSDPLEL 200
QY 181 VWTGTSVTPSRLLPTEPPSSVAEFSEATAEITVSTFNKVFTTETSRSITTSRKESDSPAGP 240
    |||
Db 201 VWTGTSVTPSRLLPTEPPSSVAEFSEATAEITVSTFNKVFTTETSRSITTSRKESDSPAGP 260
QY 241 ARQYTTKGN 249
    |||
Db 261 ARQYTTKGN 269
```

RESULT 2

```
Q9HCN6 PRELIMINARY; FRT; 620 AA.
AC Q9HCN6;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Platelet glycoprotein VI-3.
GN GPVI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20483673; PubMed=11027634;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI.";
RL Biochem. Biophys. Res. Commun. 277:27-36(2000).
DR EMBL; AB043821; BAB12247.1; -.
DR HSSP; P43626; INKR.
DR Genew; HGNC:14388; GP6.
DR InterPro; IPR003599; IG.
DR Pfam; PF0047; IG_2.
DR SMART; SMC0409; IG_2.
SQ SEQUENCE 620 AA; 67308 MW; FEBE64C55F679615 CRC64;
```

Query Match 95.6%; Score 1247; DB 4; Length 620;
Best Local Similarity 100.0%; Pred. No. 8.6e-106;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 QSGPLPKPSLQALPSSSLVPLEKPVTLRCQSPGVLDLYRLEKLSSSSRYPQDAVLFIIPAMKR 60
    |||
Db 21 QSGPLPKPSLQALPSSSLVPLEKPVTLRCQSPGVLDLYRLEKLSSSSRYPQDAVLFIIPAMKR 80
QY 61 SLAGRYRCGYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCCQTRYGF 120
    |||
Db 81 SLAGRYRCGYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCCQTRYGF 140
QY 121 DQFALYKEGDPAPYKMPERWYRASFPITVTAHSGTYRCYSSSRDPYLWSAPSDPLEL 180
    |||
Db 141 DQFALYKEGDPAPYKMPERWYRASFPITVTAHSGTYRCYSSSRDPYLWSAPSDPLEL 200
QY 181 VWTGTSVTPSRLLPTEPPSSVAEFSEATAEITVSTFNKVFTTETSRSITTSRKESDSPAG 239
    |||
Db 201 VWTGTSVTPSRLLPTEPPSSVAEFSEATAEITVSTFNKVFTTETSRSITTSRKESDSPAG 259
```

RESULT 3

```
Q9HCN7 PRELIMINARY; PRT; 321 AA.
AC Q9HCN7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Platelet glycoprotein VI-2.
GN GPVI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20483673; PubMed=11027634;
RA Ezumi Y., Uchiyama T., Takayama H.;
RT "Molecular cloning, genomic structure, chromosomal localization, and
RT alternative splice forms of the platelet collagen receptor
RT glycoprotein VI.";
RL Biochem. Biophys. Res. Commun. 277:27-36(2000).
DR EMBL; AB043820; BAB12246.1; -.
DR HSSP; P43626; INKR.
DR InterPro; IPR003599; IG.
DR Pfam; PF0047; IG_2.
DR SMART; SMC0409; IG_2.
SQ SEQUENCE 321 AA; 35158 MW; 93FBF08945958345 CRC64;
```

Query Match 91.6%; Score 1194; DB 4; Length 321;
Best Local Similarity 92.8%; Pred. No. 2.6e-101;
Matches 231; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

```
QY 1 QSGPLPKPSLQALPSSSLVPLEKPVTLRCQSPGVLDLYRLEKLSSSSRYPQDAVLFIIPAMKR 60
    |||
Db 21 QSGPLPKPSLQALPSSSLVPLEKPVTLRCQSPGVLDLYRLEKLSSSSRYPQDAVLFIIPAMKR 80
QY 61 SLAGRYRCGYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCCQTRYGF 120
    |||
Db 81 SLAGRYRCGYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVTLCCQTRYGF 140
QY 121 DQFALYKEGDPAPYKMPERWYRASFPITVTAHSGTYRCYSSSRDPYLWSAPSDPLEL 180
    |||
Db 141 DQFALYKEGDPAPYKMPERWYRASFPITVTAHSGTYRCYSSSRDPYLWSAPSDPLEL 200
QY 181 VWTGTSVTPSRLLPTEPPSSVAEFSEATAEITVSTFNKVFTTETSRSITTSRKESDSPAGP 240
    |||
Db 201 VWT-----EFSEATAEITVSTFNKVFTTETSRSITTSRKESDSPAGP 242
QY 241 ARQYTTKGN 249
    |||
Db 243 ARQYTTKGN 251
```

RESULT 4

```
Q8MUZ2 PRELIMINARY; PRT; 481 AA.
AC Q8MUZ2;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Leukocyte immunoglobulin-like receptor e.
GN LIRE.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21555186; PubMed=11698452;
RA Canavez F.C., Young N.T., Guehlein L.A., Rajalingam R., Krakoo S.;
```



```
RA Liu W.R., Kim J., Nwankwo C., Ashworth L.K., Arm J.P.;  
RT "Genomic organization of the human leukocyte immunoglobulin-like  
RT receptors within the leukocyte receptor complex on chromosome  
RT 19q13.4.";  
RL Immunogenetics 51:659-669(2000).  
DR EMBL; AF189768; AAG02024.1; -.  
DR InterPro; IPR003006; Ig_MHC.  
DR Pfam; PF00047; Ig; 2.  
KW Receptor.  
SQ SEQUENCE 448 AA; 49328 MW; 9831CC446CEA1993 CRC64;  
  
Query Match 32.1%; Score 418; DB 4; Length 448;  
Best Local Similarity 44.2%; Pred. No. 6e-30;  
Matches 95; Conservative 27; Mismatches 79; Indels 14; Gaps 2;  
  
CY 1 QSGPLPKPSIQALPSSLVPLEKPVTLRCQGPVGLYRLKLSRRYQD-----CA 51  
DB 22 QAGPLPKPTLMAEPGVSISWNSVTIWCGGTLEAREYRLDKESPAPWDRQNPLEPKKA 81  
CY 52 VLFIPAMKRSLAGRYRCSYQNSLMSLPDQLELVATGVFAKPSLSAQGPFAVSSGGDYT 111  
DB 82 RFSIPSMTEGYAGRYRCSYSPVGSQSPDLELVMTGAYSKPTLSALPSPLVTSKSVT 141  
CY 112 LCCQTRYGFQFALYKEGDPAPY----KNPERWYRASFPITVTAHSGTYRCYSFSSR 166  
DB 142 LCCQSRSPMDTFLIKERAHPDLHLRSEHGAQCHQAEFPMSPVTSVHGTYRCFSSHG 201  
CY 167 EPLYMSAPSDPLELVVTGTSVTFSRPLTEPPSSVA 201  
DB 202 SHYLSHPSDPLELVSGSLGCPSPSTRSVSTAA 236  
  
RESULT 8  
Q8N1C7 PRELIMINARY; PRT; 448 AA.  
ID Q8N1C7  
AC Q8N1C7;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Leukocyte immunoglobulin-like receptor, subfamily B (With TM and ITM  
DE domains), member 4.  
CS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
CX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC026309; AAH26309.1; -.  
DR InterPro; IPR003006; Ig_MHC.  
DR Pfam; PF00047; Ig; 2.  
KW Receptor.  
SQ SEQUENCE 448 AA; 49303 MW; A6155D29E7D89812 CRC64;  
  
Query Match 32.1%; Score 418; DB 4; Length 448;  
Best Local Similarity 44.2%; Pred. No. 6e-30;  
Matches 95; Conservative 27; Mismatches 79; Indels 14; Gaps 2;  
  
CY 1 QSGPLPKPSIQALPSSLVPLEKPVTLRCQGPVGLYRLKLSRRYQD-----CA 51  
DB 22 QAGPLPKPTLMAEPGVSISWNSVTIWCGGTLEAREYRLDKESPAPWDRQNPLEPKKA 81  
CY 52 VLFIPAMKRSLAGRYRCSYQNSLMSLPDQLELVATGVFAKPSLSAQGPFAVSSGGDYT 111  
DB 82 RFSIPSMTEGYAGRYRCSYSPVGSQSPDLELVMTGAYSKPTLSALPSPLVTSKSVT 141  
CY 112 LCCQTRYGFQFALYKEGDPAPY----KNPERWYRASFPITVTAHSGTYRCYSFSSR 166  
DB 142 LCCQSRSPMDTFLIKERAHPDLHLRSEHGAQCHQAEFPMSPVTSVHGTYRCFSSHG 201  
CY 167 EPLYMSAPSDPLELVVTGTSVTFSRPLTEPPSSVA 201  
DB 202 SHYLSHPSDPLELVSGSLGCPSPSTRSVSTAA 236
```

```
DB 202 SHYLSHPSDPLELVSGSLGCPSPSTRSVSTAA 236  
  
RESULT 9  
Q75021 PRELIMINARY; PRT; 448 AA.  
ID Q75021  
AC Q75021;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Leukocyte immunoglobulin-like receptor-5.  
GN LIR-5.  
OS Homo sapiens (Human).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
CX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Borges L., Hsu M.-L., Fanger N., Kubin M., Cosman D.;  
RL J. Immunol. 0:0-0(1997).  
DR EMBL; AF025532; AAB87666.1; -.  
DR HSSP; P43626; INKR.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003006; Ig_MHC.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; Ig; 1.  
SQ SEQUENCE 448 AA; 49325 MW; 76D1E0B7AD3A1399 CRC64;  
  
Query Match 32.1%; Score 418; DB 4; Length 448;  
Best Local Similarity 44.2%; Pred. No. 6e-30;  
Matches 95; Conservative 27; Mismatches 79; Indels 14; Gaps 2;  
  
CY 1 QSGPLPKPSIQALPSSLVPLEKPVTLRCQGPVGLYRLKLSRRYQD-----CA 51  
DB 22 QAGPLPKPTLMAEPGVSISWNSVTIWCGGTLEAREYRLDKESPAPWDRQNPLEPKKA 81  
CY 52 VLFIPAMKRSLAGRYRCSYQNSLMSLPDQLELVATGVFAKPSLSAQGPFAVSSGGDYT 111  
DB 82 RFSIPSMTEGYAGRYRCSYSPVGSQSPDLELVMTGAYSKPTLSALPSPLVTSKSVT 141  
CY 112 LCCQTRYGFQFALYKEGDPAPY----KNPERWYRASFPITVTAHSGTYRCYSFSSR 166  
DB 142 LCCQSRSPMDTFLIKERAHPDLHLRSEHGAQCHQAEFPMSPVTSVHGTYRCFSSHG 201  
CY 167 EPLYMSAPSDPLELVVTGTSVTFSRPLTEPPSSVA 201  
DB 202 SHYLSHPSDPLELVSGSLGCPSPSTRSVSTAA 236  
  
RESULT 10  
Q8MJ23 PRELIMINARY; PRT; 631 AA.  
ID Q8MJ23  
AC Q8MJ23;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Leukocyte immunoglobulin-like receptor d.  
GN LIRD.  
CS Pan troglodytes (Chimpanzee).  
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Pan.  
CX NCBI_TaxID=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21555186; PubMed=11698452;  
RA Caravez F.C., Young N.T., Guehlein L.A., Rajalingam R., Krakoo S.I.,  
RA Shum B.-P., Parham P.;  
RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes  
RT reveals framework and rapidly evolving genes.";  
RL J. Immunol. 167:5786-5794(2001).  
DR EMBL; AF383168; AAL31877.1; -.  
DR InterPro; IPR003599; Ig.
```


DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_YHC.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IGc2; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 631 AA; 69456 MW; 10E73706D2B4DEEF CRC64;

Query Match 31.9%; Score 415.5; DB 6; Length 631;
Best Local Similarity 38.1%; Pred. No. 1.6e-29;
Matches 101; Conservative 44; Mismatches 101; Indels 19; Gaps 6;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLEKLSSGRYQD-----CA 51
DB 22 QAGPFPKPTLMAEPGSAVIRGSPVTIMCQGNLEAQEYCLYKEGSTPEPMDKTNPLETRNKA 81
QY 52 VLFTPAKRSILAGRYRCSYONGSLWLSPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVT 111
DB 82 RFSIPSMTHQHHAGRYRCYRRSPAGMSPEPDPLELVVTGYFSKPTLSALPSPVVASSGQNT 141
QY 112 LQCCTRYGFDQFALYKED--PAPYKNPE--RWYRASFPITVTAHSGTYRCYSFSS 165
DB 142 LRCGSGKGYDHFVLMKEGHEQLPRILDSQQLHSGGFQALFPVGPVPSHRWTFRCYVYT 201
QY 166 RDPYLWASPSDPLELVVTGTSVTPSRILPTEPSSVAEFSEATAEL--TVSFTNKVFTTET 223
DB 202 YNDQVWSHRPSDPLELPFGVSRKFSLLTLQGP-VLARGESLTLQCGSDVGYDRFVLKESG 260
QY 224 SRSITTSPEKESDSPAGPARQYVTKG 248
DB 261 ERDPLQRPGQGPQ-AGLSQANFTLG 284

RESULT 11
ID Q8MJ25 PRELIMINARY; PRT; 645 AA.
AC Q8MJ25;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Leukocyte immunoglobulin-like receptor b.
GN LIRB.
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
CX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21555186; PubMed=11698452;
RA Canavez F.C., Young N.T., Guechlein E.A., Rajalingam R., Khakoo S.I.,
RA Shum B.P., Parham P.;
RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes
RT reveals framework and rapidly evolving genes.";
RL J. Immunol. 167:5786-5794(2001).
DR EMBL; AF383166; AAL31875.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_YHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00408; IGc2; 3.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 645 AA; 69898 MW; AC32ED6BDE8FB144 CRC64;

Query Match 31.3%; Score 408.5; DB 6; Length 645;
Best Local Similarity 39.6%; Pred. No. 7.3e-29;
Matches 106; Conservative 34; Mismatches 103; Indels 25; Gaps 8;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVD--LYRLEKLS--SRVQDAV--- 52

DB 22 QAGTLPKPTLRAEPDVSITQSGSPVTLRCQGSLEAQENHLYREKKSASWIKRIQPVYKKG 81
QY 53 -LFIPAMKRSILAGRYRCSYONGSLWLSPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVT 111
DB 82 QFIPSIWHEHAGRYRCYRRSQWSPEPDPPELVVTGAYSKPTLSALPSPVVSSGGVVT 141
QY 112 LQCCTRYGFDQFALYKEDDPAPYKNPE-----RWYRASFPITVTAHSGTYRCYS 162
DB 142 LQCGSQLAFGGFTLCKEGSD--EHPQCVNSQSHTLQMSWALFVSGVSPSRWSYRCYG 198
QY 163 FSSRDPYLWASPSDPLELVVTGTSVTPSRILPTEPSSVAEFSEATAEL--TVSFTNKVFT 220
DB 199 YDWSSPYVWLSLPSGLLELVPGVSKRS-LSVQFQPVVAPEILTLQCGSDVGYDRFVLV 257
QY 221 TETSRTTSPEKESDSPAGPARQYVTKG 248
DB 258 KEGERDFQLPGRQPQ-AGLSQANFTLG 284

RESULT 12
ID O15471 PRELIMINARY; PRT; 631 AA.
AC O15471;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Monocyte inhibitory receptor precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Arm U.P., Nwankwo C., Austen K.F.;
RT "Molecular identification of a novel family of human immunoglobulin
RT superfamily members that possess immunoreceptor tyrosine-based
RT inhibitory motifs and homology to the mouse gp49B1 inhibitory
RT receptor.";
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RX EMBL; U91528; AAB68668.1; -.
DR HSSP; P43626; INKR.
DR Genew; HGNC:6607; LILRB3.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-Like.
DR InterPro; IPR003006; Ig_YHC.
DR InterPro; IPR00734; Lipase.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Receptor; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 631 MONOCYTE INHIBITORY RECEPTOR.
SQ SEQUENCE 631 AA; 69386 MW; 61CF1967B308D79FA CRC64;

Query Match 31.1%; Score 405.5; DB 4; Length 631;
Best Local Similarity 37.0%; Pred. No. 1.3e-28;
Matches 98; Conservative 40; Mismatches 108; Indels 19; Gaps 6;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPVGVDLYRLEKLSSGRYQD-----CA 51
DB 22 QAGPFPKPTLMAEPGSAVIRGSPVTIMCQGSLEAQEYRLDKEGSPPELDRNP2LEPRNKA 81
QY 52 VLFTPAKRSILAGRYRCSYONGSLWLSPSDQLELVATGVFAKPSLSAQPGPAVSSGGDVT 111
DB 82 RFSIPSMTHQHHAGRYRCHYSSAGMSPEPDPLELVMTGTFYKPTLSALPSPVVASSGQNT 141
QY 112 LQCCTRYGFDQFALYKED--PAPYKNPE--RWYRASFPITVTAHSGTYRCYSFSS 165
DB 142 LRCGSGKGYDHFVLMKEGHEQLPRILDSQQLHSGGFQALFPVGPVPSHRWTFRCYVYT 201
QY 166 RDPYLWASPSDPLELVVTGTSVTPSRILPTEPSSVAEFSEATAEL--TVSFTNKVFTTET 223

DR InterPro; IPR003599; IG.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_3.
DR SMART; SMC0409; IG_4.
DR SMART; SMC0408; IGC2; 2.
KM Immunoglobulin domain; Receptor.
SQ SEQUENCE 643 AA; 70534 MW; BEEBC8F940B5E765AC CRC64;

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 30.78; | Score 430; | DB 6; | Length 643; |
| Best Local Similarity | 44.28; | Pred. No. 4.4e-28; | | |
| Matches 91; | Conservative 27; | Mismatches 74; | Indels 14; | Gaps 2; |

[illegible]

Search completed: November 10, 2003, 06:15:00
Job time : 37 secs

UC5897
killer cell inhibitory receptor p91 precursor - human
C/Species: Homo sapiens (man)
C/Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999
C/Accession: UC5897
R/Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Oya
J. Biochem. 123, 358-368, 1998
A/Title: Genomic structures and chromosomal location of p91, a novel murine regulatory
A/Reference number: UC5894; MUID:98218758; PMID:9538215
A/Accession: UC5897
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-466 <YAM>
A/Cross-references: GB:AF041034; NID:g2791689; PID:AA96926.1; PID:g2791690
C/Comment: This protein function as inhibitory cell-surface molecule against cell activa
C/Genetics:
A/Map position: 19q13.3-13.4
F/1-23/Domain: signal sequence #status predicted <SIG>

Query Match 29.2%; Score 381; DB 2; Length 466;
Best Local Similarity 38.2%; Pred. No. 1.8e-22;
Matches 102; Conservative 37; Mismatches 104; Indels 24; Gaps 8;

QY 1 QSGPLPKPSIQALPSSLVPLEKPVTLRCQGPVGD---LYPLEKLS--SRYQD--QAV 52
DB 22 QAGHLPKPTLWAPGSVIIQCSPTLRCQSLQASEYHLYRENKKSASWYRRCQPKNQ 81

QY 53 FIFPMKSLAGRYRCSYONGSIMSLPSDQLELVATGVFAKPSLSAQCPAVSSGGV 112
DB 32 FPIPTWEHAGRYHCQYSHNSSEYSDPLELVTVGAYSKPTLSALPSVTVLGGV 141

QY 113 QCCTRYGPDQFALYKEDPAFYKPERW-----YRASPIITVTAHSGTYRCYSF 163
DB 142 QCVSQVAFDGFILCKEGED---EHPQLNLSHSHARGSSRAIFSVGFSNRRWSHRCY 198

QY 164 SSRDPYLMASPSDPLELVTVGTSVTPSRLPTEPPSSVAEFSATAEIT--VSFTNKVTT 221
DB 199 DINSPIYVWSSPSDPLELVTVGTSVSKKPS-LSVQGFVVAFGESITLQCVSDVGYDRFVLYK 257

QY 222 ETSRSITTSFKESDSPAGPARCYTKG 248
DB 258 EGERDRLQLPGRFQ-AGLSQANFTLG 283

RESULT 3
146020
Fc gamma 2 receptor precursor - bovine
C/Species: Bos primigenius taurus (cattle)
C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999
C/Accession: 146020; S53115
R/Zhang, G.; Young, J.R.; Tregaskes, C.A.; Sopp, P.; Howard, C.J.
J. Immunol. 155, 1534-1541, 1995
A/Title: Identification of a novel class of mammalian Fc gamma receptor.
A/Reference number: 146020; MUID:95363119; PMID:7636215
A/Accession: 146020
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-264 <ZHA>
A/Cross-references: EMBL:Z37506; NID:g732571; PID:CAA65736.1; PID:g732572
C/Keywords: immunoglobulin receptor

Query Match 28.8%; Score 375; DB 2; Length 264;
Best Local Similarity 42.1%; Pred. No. 2.7e-22;
Matches 85; Conservative 29; Mismatches 68; Indels 20; Gaps 4;

QY 1 QSGPLPKPSIQALPSSLVPLEKPVTLRCQGPVGDLYRLEKLS--RYQDQ 51
DB 22 QAGHLPKPTLWAPGSVIIQCSPTLRCQSLQASEYHLYRENKKSASWYRRCQPKNQ 81

QY 52 VLFPMKSLAGRYRCSYONGSIMSLPSDQLELVATG-----VFAKPSLSAQCPAVS 105
DB 82 NFPISTVREGQAGRYHCHSHFGVWMSPESEPLDLVAGEFPAGRLDRPSVSRPSPVA 141

QY 106 SGGDVTLQCCTRYGPDQFALYKED---DPAPYKPER--YRASPIITVTAHSGTYRC 160
DB 142 PGENVTILCQSGNRITFLSKEGAAHRLRLRSODQDGYQAEFSLSPVTSAGCTYRC 201

QY 161 YSFSSRDPLYMSAPSDPLELV 182
DB 202 YRSLSTNPYLLSQSPSDLLLV 223

RESULT 4
UC5894
killer cell inhibitory receptor p91A precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 17-Mar-1999
C/Accession: UC5894
R/Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.;
J. Biochem. 123, 358-368, 1998
A/Title: Genomic structures and chromosomal location of p91, a novel murine regula
A/Reference number: UC5894; MUID:98218758; PMID:9538215
A/Accession: UC5894
A/Status: nucleic acid sequence not shown
A/Molecule type: DNA
A/Residues: 1-841 <YAM>
A/Cross-references: GB:AF040946
C/Comment: This protein function as inhibitory cell-surface molecule against cell ac
C/Genetics:
A/Map position: 7
F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-841/Product: killer cell inhibitory receptor p91A #status predicted <MAT>
F/24-118,119-220,221-315,316-418,419-517,518-618/Domain: extracellular Ig-like #stat
F/636-674/Domain: transmembrane #status predicted <TM>
F/675-765/Domain: cytoplasmic #status predicted <CYT>

Query Match 28.6%; Score 372.5; DB 2; Length 841;
Best Local Similarity 38.5%; Pred. No. 1.8e-21;
Matches 80; Conservative 35; Mismatches 76; Indels 17; Gaps 3;

QY 2 SGPPLPKPSIQALPSSLVPLEKPVTLRCQGPVGDLYRLEKLS--RYQDQAVL----- 53
DB 220 SGNLCKPTITKAEPGSVITSRKAMTIWCCQNLDAEVYFLHNEGSKTOSTQTLLQPPKMK 279

QY 54 -FIFPMKSLAGRYRCSYONGSIMSLPSDQLELVATGVFA--KPSLSAQCPAVSSGGV 110
DB 280 FPIPTWEHAGRYHCQYSHNSSEYSDPLELVTVGAYSKPTLSALPSVTVLGGV 141

QY 111 TLCCQTRYGPDQFALYKED-----DPAPYKPERYRASPIITVTAHSGTYRCYSF 164
DB 340 TLHCASDFHDKFILTKEKKGNSLDTEHIISSRQYRALFIIGPTTHTGTFRCYGF 399

QY 165 SRDPYLMASPSDPLELVTVGTSVTPSRL 192
DB 400 KNAPQLMSVPSDPLQITLISGLSKKPSLL 427

RESULT 5
UC5896
killer cell inhibitory receptor p91C precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999
C/Accession: UC5896
R/Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.;
J. Biochem. 123, 358-368, 1998
A/Title: Genomic structures and chromosomal location of p91, a novel murine regula
A/Reference number: UC5894; MUID:98218758; PMID:9538215
A/Accession: UC5896
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-635 <YAM>
A/Cross-references: GB:AF041036; NID:g2791693; PID:AA96928.1; PID:g2791694
C/Comment: This protein function as inhibitory cell-surface molecule against cell ac
F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-118,119-220,221-315,316-418,419-517,518-618/Domain: extracellular Ig-like #stat

Query Match 28.0%; Score 365.5; DB 2; Length 635;
Best Local Similarity 37.5%; Pred. No. 4.4e-21;
Matches 78; Conservative 38; Mismatches 75; Indels 17; Gaps 3;
QY 2 SGFLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLKLISSSRVQDQAVL-----53
Pb 220 SGNLQKPTIKAEPPGSVIAASKRAMTWCQNLDAEVYFLHNEGSKTOSTOCTLOQFGYKGR 279
QY 54 -FIPAKRSLAGRYRCYQNGSLWSPSDQLELVATGVFA--KPSLSAQPGPAVSSGGDV 110
Db 280 FFIPSVTQOHAGQRCYCYSSAGWSQPSDTELVVTGTYEHYKPRLSVLPSPVVTAGGMM 339
QY 111 TLQCTRYGFDQFALYKGD-----PAPYKNPERKVRASFPITVTAAHSGTYRCYSFS 164
Db 340 TLHCASDPHYDKFILTKECKKFGNSLDTEHIISSSRQYRALFTIGPTTPTHTGTTRCYGYF 399
QY 165 SRDPYIWSAPSDPLELVVTGTSVTPSR 192
Db 400 KNAPQLWSVPSDLQQLILISGLSKKPSLL 427

RESULT 6

CS5895
killer cell inhibitory receptor p91B precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999
C/Accession: J05895
R/Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Chya
J. Biochem. 123, 358-368, 1998
A/Title: Genomic structures and chromosomal location of p91, a novel murine regulatory r
A/Reference number: J05894; MIMD:98218758; PMID:9538215
A/Accession: J05895
A/Status: nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-680 <YAY>
A/Cross-references: GB:AF041035; NID:g2791691; P/EN:AAB96927.1; PID:g2791692
C/Comment: This protein function as inhibitory cell-surface molecule against cell activa
C/Genetics:
A/Map position: 7
F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-118,119-220,221-315,316-418,419-517,518-618/Domain: extracellular Ig-like #status p
F/636-674/Domain: transmembrane #status predicted <TM>
F/675-680/Domain: cytoplasmic #status predicted <CYT>

Query Match 26.5%; Score 345.5; DB 2; Length 680;
Best Local Similarity 36.1%; Pred. No. 1.8e-19;
Matches 75; Conservative 39; Mismatches 77; Indels 17; Gaps 3;
QY 2 SGFLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLKLISSSRVQDQAVL-----53
Pb 220 SGNLQKPTIKAEPPGSVIAASKRAMTWCQNLDAEVYFLHNEGSKTOSTOCTLOQFGYKGR 279
QY 54 -FIPAKRSLAGRYRCYQNGSLWSPSDQLELVATGVFA--KPSLSAQPGPAVSSGGDV 110
Db 280 FFIPSVTQOHAGQRCYCYSSAGWSQPSDTELVVTGTYEHYKPRLSVLPSPVVTAGGMM 339
QY 111 TLQCTRYGFDQFALYKGD-----PAPYKNPERKVRASFPITVTAAHSGTYRCYSFS 164
Db 340 TLHCASDPHYDKFILTKECKKFGNSLDTEHIISSSRQYRALFTIGPTTPTHTGTTRCYGYF 399
QY 165 SRDPYIWSAPSDPLELVVTGTSVTPSR 192
Db 400 KNAPQLWSVPSDLQQLILISGLSKKPSLL 427

RESULT 7

G01925
KIR (cl-11) NK receptor precursor protein - human
C/Species: Homo sapiens (man)
C/Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999
C/Accession: G01925; I61726
R/Magtmann, N.
submitted to the EMBL Data Library, June 1995

A/Reference number: G08782
A/Accession: G01925
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-444 <WAG>
A/Cross-references: EMBL:U30274; NID:g1004360; PIDN:AAB52522.1; PID:g1004361
R/Colonna, V.; Samaridis, J.
Science 268, 405-408, 1995
A/Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA
A/Reference number: A56247; MIMD:95232526; PMID:7716543
A/Accession: I61726
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-444 <RES>
A/Cross-references: GB:L41269; NID:g780307; PIDN:AAA69870.1; PID:g780308
C/Genetics:
A/Gene: NKAT-3
A/Map position: 19

Query Match 24.6%; Score 320.5; DB 2; Length 444;
Best Local Similarity 38.6%; Pred. No. 9.9e-18;
Matches 83; Conservative 22; Mismatches 81; Indels 29; Gaps 5;

QY 7 KPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLKLISSSRVQDQAV-----LFI 55
Db 123 KPSLHAPGPLVKSGRVILQWSDIMEHFLLHKEGISKDPRLVGCIHGVSKANFSI 182
QY 56 PAKRSIAGRYRC-----SYQNGSLWSPSDQLELVATGVFAKPSLSAQPGPAVSSGG 108
Db 183 GPMMLALAGTYRCYGSVTHTPYQ----LSAPSDPDIIVTGPYKPSLSAQPGPAVQAGE 238
QY 109 DVTLCQCTRYGFDQFALYKGDPAFYKNP----ERWYRASFPITVTAAHSGTYRCYSF 163
Db 239 SVTLSCSSRSSYDWHLSREGAHERRLPAVRKVMRTFQADPFL--GPATHGTYRCYGS 296
QY 164 SSRDPYIWSAPSDPLELVVTGTSVTPSR 198
Db 297 FRHSPYEMSDPSDPLVSVTGNPSSSWPSPTEPSS 331

RESULT 8

B53434
cell surface glycoprotein gp49B form 2 precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 05-Nov-1999
C/Accession: B53434
R/Castells, M.C.; Wu, X.; Arm, J.P.; Auster, K.F.; Katz, H.R.
J. Biol. Chem. 269, 8393-8401, 1994
A/Title: Cloning of the gp49B gene of the immunoglobulin superfamily and demonstratio
A/Reference number: A53434; MIMD:94179223; PMID:8132564
A/Accession: B53434
A/Status: preliminary
A/Molecule type: DNA; mRNA
A/Residues: 1-296 <CAS>
A/Cross-references: GB:U05265; NID:g475446; PIDN:AAA17798.1; PID:g475448; GB:U05266;
C/Genetics:
A/Gene: gp49B
A/Introns: 12/3; 24/2; 119/2; 220/1; 232/1; 249/3; 272/1
C/Keywords: alternative splicing; glycoprotein

Query Match 24.1%; Score 314.5; DB 2; Length 296;
Best Local Similarity 35.5%; Pred. No. 1.8e-17;
Matches 81; Conservative 33; Mismatches 93; Indels 21; Gaps 5;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPFGVDLYRLKLISSSRVQD-----QA 51
Db 22 QAGHLPKPIIWAEPGSVIAATYVITWQGSWEAQYHLYKEKSVNPDTCVPLFTRKKA 81
QY 52 VLFIPAKRSLAGRYRCYQNGSLWSPSDQLELVATGVFAKPSLSAQPGPAVSSGGDV 111
Db 82 KFNIPSMITSYAGTYKCYESAAGFSEHSDAMELVMTGAYENPSLSYTPSSNVTSSYGIS 141
QY 112 LQCTRYGFDQFALYKGD-----DAFYKNPERKVRASFPITVTAAHSGTYRCYSF 163

Db 142 FSCSSSIVFGRIILQEGHGLSWTLDSQHGANQPSY--ATFVLDAVTNHNHNGTFRGCGY 199

QY 164 SSRDPYLWSAPSDPLELVVTGTSVTPSRIFCTEPSSVAEF-SEATAEL 210

Db 200 FRNEPQWMSKPSNSLDLMISETK-DQSSITPTEDDASVKNITQSENNAEL 246

RESULT 3

A56247

Natural killer cell-associated protein - human

C:Species: Homo sapiens (man)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

C:Accession: A56247

R:Colonna, M.; Samaridis, J.

Science 268, 405-408, 1995

A:Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B

A:Reference number: A56247; NCID:95232526; PMID:7716543

A:Accession: A56247

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-348 <RES>

A:Cross-references: GB:U41267; NID:g780303; PIDN:AAA69869.1; PID:g780304

C:Genetics:

A:Gene: GDB:NKAT1

A:Cross-references: GDB:698165

A:Map position: 19

Query Match 24.1%; Score 314; DB 2; length 348;
Best local similarity 32.3%; Pred. No. 2.4e-17;
Matches 93; Conservative 36; Mismatches 105; Indels 54; Gaps 10;

QY 7 KPQLQALPSSSLVPLEKPYTLRCQGPVGLYRLKLSRRYQD-----QAVL 53

Db 28 KPQLAHFGLVSEETVILQCMWDVMEHFLHR--EGFNDTLRLIGEHHDGVSKANF 85

QY 54 FIFAMKRSIAGRYRC-----SYQNGSLMSLPDQLELVATGVFAKPSLSAQPGPAVSS 106

Db 86 SISRTQDLAAGTYRCYGVSVTHSPYQ---VSAPSDPLDIVITGLYKPSLSAQPGPTVLA 141

QY 107 GGDVTLQCCQTRYGFDQFALYKGDPAFYKNP----ERWYRASFPITVTAAHSGTYRCY 161

Db 142 GENVTLSGSSRSSYDMYHLSREGAHERRLPAGPKXNGTFQADFP--GPATHGTYRCF 199

QY 162 SFSSRDPLYWSAPSDPLELVVTGTSVTPSRILPTEPSSVA----EFSEATAELTVSF-- 214

Db 200 GSFHDSPEWMSKSSDPLVSVTGNPNSGWPSPTEPSSKTNPRHLHLIGTSVAILFIJ 259

QY 215 -----TNK---VFTTETSRISITSPKESDSPAGPARQYITKGN 249

Db 260 LFFLLHRCMSNKNAAVMDQESAGNRTANSEDSDE-CDPQEVITYQLN 306

RESULT 10

I61725

Natural killer associated transcript 2 - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999

C:Accession: I61725

R:Colonna, M.; Samaridis, J.

Science 268, 405-408, 1995

A:Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B

A:Reference number: A56247; NCID:95232526; PMID:7716543

A:Accession: I61725

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-341 <RES>

A:Cross-references: GB:U41268; NID:g780305; PIDN:AAA69869.1; PID:g780306

C:Genetics:

A:Gene: NKAT-2

Query Match 24.0%; Score 312.5; DB 2; length 341;
Best local similarity 37.4%; Pred. No. 3.1e-17;

Matches 82; Conservative 24; Mismatches 76; Indels 37; Gaps 7;

QY 7 KPQLQALPSSSLVPLEKPYTLRCQGPVGLYRLKLSRRYQD-----QAVL 53

Db 28 KPQLAHFGLVSEETVILQCMWDVMEHFLHR--EGFKDTLRLIGEHHDGVSKANF 85

QY 54 FIFAMKRSIAGRYRC-----SYQNGSLMSLPDQLELVATGVFAKPSLSAQPGPAVSS 106

Db 86 SIGPMQDLAAGTYRCYGVSVTHSPYQ---VSAPSDPLDIVITGLYKPSLSAQPGPTVLA 141

QY 107 GGDVTLQCCQTRYGFDQFALYKGDPAFYKNP----ERWYRASFPITVTAAHSGTYR 159

Db 142 GESVTLSGSSRSSYDMYHLSREGAHERRLPAGPKXNGTFQADFP--GPATHGTYR 197

QY 160 CYSFSSRDPLYWSAPSDPLELVVTGTSVTPSRILPTEPSS 198

Db 198 CFGSFRDSPYEWMSNSDPLVSVTGNPNSGWPSPTEPSS 236

RESULT 11

G01924

KIR (cl-2) NK receptor precursor - human

N:Alternate names: killer cell inhibitory receptor

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 05-Nov-1999

C:Accession: G01924; G01945

R:Wagtmann, N.

submitted to the EMBL Data Library, June 1995

A:Reference number: G08780

A:Accession: G01924

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-444 <WAG>

A:Cross-references: EMBL:U30273; NID:g1004358; PIDN:AA52521.1; PID:g1004359

R:D'Andrea, A.; Chang, C.; Franca-Bacon, K.; McClanahan, T.; Phillips, J.H.; Janier, I.

submitted to the EMBL Data Library, July 1995

A:Reference number: G08908

A:Accession: G01945

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-444 <DXA>

A:Cross-references: EMBL:U31416; NID:g973405; PIDN:AA023725.1; PID:g973406

C:Genetics:

A:Gene: NKBI

Query Match 24.0%; Score 312.5; DB 2; length 444;
Best local similarity 38.1%; Pred. No. 4.2e-17;
Matches 82; Conservative 22; Mismatches 82; Indels 29; Gaps 5;

QY 7 KPQLQALPSSSLVPLEKPYTLRCQGPVGLYRLKLSRRYQDQAV-----LFI 55

Db 123 KPQLAHFGLVKSGERVILQCMWDVMEHFLHKEGISKPSRLVQGIHDGVSKANFSI 182

QY 56 PAMKRSIAGRYRC-----SYQNGSLMSLPDQLELVATGVFAKPSLSAQPGPAVSSG 108

Db 183 GPMMLALAGTYRCYGVSVTHPYQ---LSAPSDPLDIVTGPYEKPSLSAQPGPKVQAGE 238

QY 109 DVTLQCCQTRYGFDQFALYKGDPAFYKNP----ERWYRASFPITVTAAHSGTYRCY 163

Db 239 SVTLSCSSRSSYDMYHLSREGAHERRLPAVRKVNRTFQADFP--GPATHGTYRCFS 296

QY 164 SSRDPYLWSAPSDPLELVVTGTSVTPSRILPTEPSS 196

Db 297 FRHSPEWMDPSDPLVSVTGNPSSSSWSPTEPSS 331

RESULT 12

G02630

FcalphaRb - human

C:Species: Homo sapiens (man)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998

C:Accession: G02630

R:van Dijk, T.B.; Morton, H.C.; Caldenhoven, E.; Bracke, M.; Raaijmakers, J.A.M.; Lan

Matches 77; Conservative 21; Mismatches 74; Indels 29; Gaps 5;

```
Oy      7 KPSLQALPSSIVPJEKPYTLRCQGPVGVLYRLEKLSRRYQDAV-----LF: 55
      123 KPSLLAHPGPLVKSGERVILQCSWDIMFEHFLHKEG:SKDPSRLVGQIHGVSXANFSI 182
Db
Oy      56 PAMKRSIAGRYRC-----SYONGSLWSLPSDQLBLVATGVFAKPSLSAQGPFAVSSGG 108
      183 GPMMLALAGTYRCYGSVTHTPYQ-----LSAPSDPLDIVTGPYEKPSLSAOPGPKVOAGE 238
Oy      109 DVTIQCCFRYGFDDQFALYKGGDPAFYKNP-----ERWYRASFPITVTAAHSGTYRCYSF 163
      239 SVTLSCSSSRSSYDWMYHLSRERGAHERLPAVRKVNRTFQADPPL--GPATHGCTYRCFGS 296
Db
Oy      164 SSRDPYLCMSAPSDP:ELVVTG 184
      297 FRHSPYEWSCPSDPLLVSVTG 317
```

Search completed: November 10, 2003, 06:20:37
Job time : 23 secs